Page

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 9, 2004, 15:26:05 ; Search time 32 Seconds (without alignments) 245.223 Million cell updates/sec Run on:

Perfect score:

US-10-768-874-2

1 MSITQSFFVLTLAIFGAASD......NWGVMKDGEKHYFTVENCQE 152 **BLOSUM62** Scoring table: Sequence:

389414 segs, 51625971 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:\* Database :

/cgm2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/B\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/PcTUS\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/pcTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2, Appli	7	'n	5,	'n	'n	Sequence 51, Appl	4,	4	4				Sequence 12086, A		107	107,	107,	107,	Sequence 107, App	101	107,	-	107,	1, Ap	'n	Ŋ,
SUMMARIES	ID	US-09-036-355A-2	US-09-702-647A-2	US-09-036-355A-5	US-09-702-647A-5	US-09-036-355A-3	US-09-702-647A-3	US-09-059-584-51	US-09-036-355A-4	US-09-702-647A-4	US-09-107-532A-4552	US-09-651-200-19	US-08-961-083-158	US-09-536-784-158	US-09-489-039A-12086	US-09-668-097A-32	US-08-487-890A-107	US-08-478-435-107	US-08-337-483-107	US-08-478-373-107	US-08-474-671-107	US-08-483-577A-107	US-08-897-438-107	US-08-637-654-107	US-08-649-518-107	US-09-608-790-1	US-09-397-885-5	US-09-969-362-5
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6/0	Query Match	100.0	100.0	73.9	73.9	15.8	15.8	10.7	10.5	10.5	10.2	9.8	9.5	9.2	0.6	8.9	8.8	8.8	8.8	8.8	8.8	8.8	8.8	•	8.8	8.7	8.7	8.7
	Score	825	825	610	610	130	130	88	87	87	84.5	0	9/	94	74	73.5	72.5	72.5	72.5	72.5	72.5				72.5	72	72	72
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Sequence 4219, Ap	Sequence 30, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 20, Appl		Sequence 5, Appli	'n	Ŋ	Ŋ	5,	2	5	2	Ŋ	-	Н
US-09-134-001C-4219 US-09-041-889-30	US-09-417-264-30	US-09-296-840A-4	US-08-793-824-2	US-09-651-200-20	US-09-543-681A-6366	US-08-487-890A-5	US-08-478-435-5	US-08-337-483-5	US-08-478-373-5	US-08-474-671-5	US-08-483-577A-5	US-08-897-438-5	US-08-637-654-5	US-08-649-518-5	US-09-397-885-1	US-09-969-362-1
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363	367	330	1577	325	365	913	913	913	913	913	913	913	913	913	923	923
8.3	8.5	8.51	8.5	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4
71.5	70.5	70	70	69.5	69.5	69.5	69.5	69.5	69.5	69.5	69.5	69.5	69.5	69.5	69	
დთ	0	런	Ç.	2	14	35	36	37	38	39	0,	1	42	53	14	5

### ALIGNMENTS

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Sequence 2, Application US/09036355A
Patent No. 6162785
GENERAL INFORMATION:
APPLICANT: Cupp, Mary S.
APPLICANT: Cupp, Eddie W.
APPLICANT: Cupp, Eddie W.
TITLE OF INVENTION: RECOMBINANT VASOACTIVE PROTEIN FROM TITLE OF INVENTION: SALIVARY GLAND OF THE BLACK FLY
                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: PLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/036,335A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 572
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         NC
USA
                                                                                                                                                                                                                                                                                                                                                                              27622
JS-09-036-355A-2
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                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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0 9 1 MSITQSFFVLTLAIRGAASDNPIADRKCIVISDGDLVMHERKPGQEFPYYVYMIPKGTEY ; 0 Length 152; Indels Query Match 100.0%; Score 825; DB 3; Best Local Similarity 100.0%; Pred. No. 4.1e-92; Matches 152; Conservative 0; Mismatches 0; 8

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1 MSITQSFFVLTLAIFGAASDNPIADRKCIVISDGDLVMHERKPGQEFPYYVYMIPKGTEY

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61 DDQRWILESVGGDHYKLKNKRSGRYLVYGTFDYFLTAGAAVREMDHFKFTADGTGKYDIS 120
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APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Cupp, Eddie W.
APPLICANT: Cupp, Eddie W.
APPLICANT: Swaim, Steven F.
TITLE OF INVENTION: RECOMBINANT VASOACTIVE PROTEIN FROM
TITLE OF INVENTION: SALIVARY GLAND OF THE BLACK FLY
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Cupp, Mary S.

APPLICANT: Ribelro, Jose M.C.

APPLICANT: Swaim, Steven F.

ITLE OF INVENTION: Recombinant Vascactive Protein from TITLE OF INVENTION: Recombinant Vascactive Protein from TITLE OF INVENTION: Salivary Gland of the Black Fly FILE REPRENCE: 35721/205407

CURRENT APPLICATION NUMBER: US/09/702,647A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 825; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.1e-92;
Matches 152; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SKANGHPRSRGKNWGVMKDGEKHYFTVENCQE 152
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                                                                                         121 SKANGHPRSRGKOWGVMKDGEKHYFTVENCOE 152
                                                                   121 SKANGHPRSRGKNWGVMKDGEKHYFTVENCQE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-036-355A-5; Sequence 5, Application US/09036355A; Patent No. 6162785
                                                                                                                                                                                                                            Sequence 2, Application US/09702647A
Patent No. 6500420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Simulium vittatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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42 KPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKLKWKFSGRYLVYGTFDYFLTAGAAV 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cupp, Mary S.
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Swalin, Steven F.
TITLE OF INVENTION: Recombinant Vasoactive Protein from TITLE OF INVENTION: Salivary Gland of the Black Fly
FILE REFERENCE: 35721/205407
CURRENT APPLICATION NUMBER: US/09/702,647A
CURRENT FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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100.0%; Pred. No. 3e-66;
iive 0; Mismatches 0
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100.0%; Pred. No. 3e-66;
tive 0; Mismatches 0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,355A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/09036355A; Patent No. 6162785; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/09702647A; Patent No. 6500420
                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5721-
TELECHONIC (ATTOR INFORMATION:
TELEPHONE: 919 420 202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Simulium vittatum
US-09-702-647A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-036-355A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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JS-09-059-584-51
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                                                                                                                                                                                                                              RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 22;
                               APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Cupp, Eddie W.
APPLICANT: Swalm, Steven F.
TITLE OF INVENTION: RECOMBINANT VASOACTIVE PROTEIN FROM
TITLE OF INVENTION: SALIVARY GLAND OF THE BLACK FLY
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Cupp, Eddie W.
APPLICANT: Cupp, Eddie W.
APPLICANT: Swaim, Steven F.
TITLE OF INVENTION: Recombinant Vasoactive Protein from TITLE OF INVENTION: Salivary Gland of the Black Fly FILE REPERENCE: 35721/205407
CURRENT APPLICATION NUMBER: US/09/702,647A
CURRENT FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: SALIVARIAN UNDER OF SECONDAN UNDER OF SEQ ID NOS: SALIVARIAN UNDER OF SEQ ID 
                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NC
COUNTRY: USA
ZIP: 27622
COMPUTER: USA
ZIP: 27622
COMPUTER: FLORDY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,335A
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 130; DB 3; I
Pred. No. 4.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICALLO...
FILING DATE:
CLASSIPICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Spruil, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5721-/
TELECOMMUNICATION INPORMATION:
TELEFRAN: 919 881 3175
TELEFRAN: 919 881 3175
TELEFRAN: 919 882 ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 GKNWGVMKDGEKHYFTVENCQE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GKNWGVMKDGEKHYFTVENCOE 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
15.8%; Soc
Best Local Similarity 100.0%; Pr
Matches 22; Conservative 0;
Cupp, Mary S.
Ribeiro, Jose M.C.
Cupp, Eddie W.
Swaim, Steven F.
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; ORGANISM: Simulium vittatum
US-09-702-647A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                    STREET: 3605 CITY: Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-09-702-647A-3
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276 MIDAKKGOSFSSF------ERRAGDRYSAMSSHEYPSLLTDDKNKPDNY 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KNKFSGR 84
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                                                                                                                                                                                                                                                                            APPLICANT: Myers, Lisa E
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Locenore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Vang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
10.7%; Score 88; DB 4; Length 712;
Best Local Similarity 27.8%; Pred. No. 0.09;
Matches 37; Conservative 10; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/059,584

FILING DATE: 14-APR-1998

CLASSIFICATION NUMBER: US/09/059,584

FILING DATE: 01-APR-1998

CLASSIFICATION NUMBER: US/09/059,584

FILING DATE: 03-JAN-1997

CLASSIFICATION NUMBER: US/09/059,584

FILING DATE: 03-JAN-1997

CLASSIFICATION NUMBER: US/09/059/059,594

FILING APPLICATION NUMBER: 24973

REFERENCY/DOCKET NUMBER: 1038-794

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1165

TELEPHONE: (416) 595-1163

INFORMATION FOR SEQ ID NO: 51: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 MHERKPGOEFPYYVYMIPKGTEYDDORWILESVGGDHYKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
131 GKNWGVMKDGEKHYFTVENCQE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   1 GKNWGVMKDGEKHYFTVENCOE 22
                                                                                                                                                                                              Sequence 51, Application US/09059584 Patent No. 6440701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-09-059-584-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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WS-09-107-532A-4552

Sequence 4552, Application US/09107532A

Patent No. 6583275

Patent No. 658275

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 VGGDHYKLKNKFSGRYL------VYGTFDYFLTAGAAVREMDHFKFTADGT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 VISDGDLVMHE-----RKPGQEFPYXV-YMI-----PKGTEYDDQR--WIL----ES 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 36; Indels 39; Gaps
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                            Query Match 10.5%; Score 87; DB 4; Length 15; Best Local Similarity 100.0%; Pred. No. 0.00045; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COPERATING SYSTEM: <UNKNOWN>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 14 July 2, 1997
ATTORIEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-8077
TELEPHONE: (781)893-8077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) NAME/KEY: misc_feature

; LOCATION: (B) LOCATION 1...1297

; SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

US-09-107-532A-4552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1297 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         42 KPGQEFPYYVYMIPK 56
                                                                                                                                                                                                                    1 KPGQEFPYYVYMIPK 15
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TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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APPLICANT: Cupp, Eddle W.C.
APPLICANT: Cupp, Eddle W.C.
APPLICANT: Cupp, Eddle W.C.
APPLICANT: Swain, Steven F.
TITLE OF INVENTION: Recombinant Vascactive Protein from
TITLE OF INVENTION: Salivary Gland of the Black Fly
FILE REPRENCE: 35721/205407
CURRENT APPLICATION NUMBER: US/09/702,647A
CURRENT FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                          GENERAL INPORMATION:
APPLICANT: Cupp, Mary S.
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Swaim, Steven F.
APPLICANT: Swaim, Steven F.
TITLE OF INVENTION: RECOMBINANT VASOACTIVE PROTEIN FROM TITLE OF INVENTION: SALIVARY GLAND OF THE BLACK FLY NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5%; Score 87; DB 3; Length 15; 100.0%; Pred. No. 0.00045; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
COTAMIN: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,355A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sprull!, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5721-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEPHONE: 919 420 2202
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09702647A Patent No. 6500420 GENERAL INFORMATION:
                                Sequence 4, Application US/09036355A
Patent No. 6162785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 KPGOEFPYYVYMIPK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KPGQEPPYYVYMIPK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Simulium vittatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide US-09-036-355A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-702-647A-4
US-09-036-355A-4
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INFORMATION F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4
LENGTH: 15
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 158, Application US/08961083

Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
                                                                                                                                                                                                   APPLICANT: Green et al TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and TITLE OF INVENTION: Lymphocyte Encoded Thereby FILE REFERENCE: 15966-56 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 60/12309
PRIOR FILING DATE: 60/103578
PRIOR FILING DATE: 60/000-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;

    Score 80.5; DB 4; Length 329;
    Pred. No. 0.24;
    Mismatches 38; Indels 27

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 ERKPGQEFPYYYYMIPKG-TEYDDQRWILESVGGDHYKLKNKFSGRY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                  RESULT 11
US-09-651-200-19
; Sequence 19, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSITOSFFVLTLAIFGAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                       1037 G-FDİ 1040
115 GKYDI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER SOFTWARE: Pate SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-961-083-158
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156 GAMMQNEWLYDPAYSAYFYLKSDGT-YANQEW--QKVGGKWYYFKKWGYMARNEWQG--- 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 ----NYYLTGSGA---MATDEVIMDGTRYIFAASGELKEKKDINVGW-VHRDGKRYPF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 VYGTFDYFLTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSRGKNWGVMKDGEKHYF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIF: 20850
COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-00-1997
CLASSIFCATION: <a href="https://doi.org/10.1007/j.chr/">CLASSIFCATION DATA:</a>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.2%; Score 76; DB 3; Length 471; Best Local Similarity 25.2%; Pred. No. 1.4; Matches 30; Conservative 19; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.2%; Score 76; DB 4; Length 471; 25.2%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PB340P3
TELECOWNUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 158: US-09-536-784-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 amino acids
TYRE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 158, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
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STRANDEDNESS: single
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SECUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Maryland
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-961-083-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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Best Local Similarity
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
RICH APPLICATION NUMBER: US/0/117,747
PRIOR APPLICATION NUMBER: US/0/117,747
PRIOR APPLICATION NUMBER: 14342
SEQ ID NO 12086
LENGTH: 429
  9
                                                                                                     156 GAMMONEWLYDPAYSAYFYLKSDGT-YANQEW--QKVGGKWYYFKKWGYMARNEWQG--- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 GDLVMHERKFGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKLK-----NKFSGRYL 86
                                                                                                                                                           87 VYGTFDYFLTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSRGKNWGVMKDGEKHYF 145
                                                                                                                                                                                               210 -----NYLIGSGA---MATDEVIMDGTRYIFAASGELKEKKDLANVGW-VHRDGKRYFF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SITQSFFVLTLAIFGAASDNPIADRKCIVISDGDLVMHERKPGQEFPYYVYMIPKGTEYD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- DNPIADRKCIVISDG--DLVMHER 41
  22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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8.9%; Score 73.5; DB 4; Length 360;
Best Local Similarity 22.9%; Pred. No. 1.9;
Matches 38; Conservative 25; Mismatches 52; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.0%; Score 74; DB 4; Length 429; Best Local Similarity 31.7%; Pred. No. 2.2; Matches 32; Conservative 16; Mismatches 37; Indels
  19; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DORWILESVGGDHYKLKNKFSGRYLVYG---TFDYFLTAGA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15

US-09-668-097A-32

Sequence 32, Application US/09668097A

PROPLICANT: Cahoon, Edgar B.

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Shan, Jennie

TITLE OF INVENTION: Plant Lipases

FILE REFERENCE: BB1401 US NA

CURRENT APPLICATION UNMER: 60/157309

PRIOR APPLICATION NUMBER: 60/157309

PRIOR FILING DATE: 1999-10-01

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ITOSFFVL-----TLAIFGAAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Triticum aestivum
  30; Conservative
                                                                                                                                                                                                                                                                                                                         US-09-489-039A-12086
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LENGTH: 360
Matches
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213 LPIGCFPLYLTLYGSSNQSDYDGDGCLRRFNDLSGYHNRLLRQGIG----RLRSKYAGVR 268
153 LSKSLFILGEFGGNDYNAAIFGGKSLDEVYTYVPHIINKVTSGVETLIGLGAVDVVVPGV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---DORWILESVGGDHYKLKNKFSGRY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:| |::|| |::|| | |::|| | | |::|| | |:::|| | | |:::|| | | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| | |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 LVYGTFDYFLTAGAAVREMDHFKFT-----ADGTGKYDISSKA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 KPGQEFPYY -- VYMIPKGTEYD --
```

Search completed: September 9, 2004, 15:32:04 Job time : 33 secs

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

September 9, 2004, 15:22:35 ; Search time 40 Seconds Run on:

(without alignments) 365.528 Million cell updates/sec

US-10-768-874-2

825 1 MSITQSFFVLTLAIFGAASD.....NWGVNKDGEKHYFTVENCQE 152 score: Sequence: Title: Perfect :

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		م/ <i>ه</i>			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
П	83.5	10.1	474	٦	876904	hypothetical prote
N	78	9.51	448	~	C98122	choline binding pr
m	78	9.5	1143	~	S46122	SNF2 protein homol
4	77	9.3	174	N	S07146	damma-s-crystallin
ហ	77	9.3	501	0	F98050	lysozyme (EC 3.2.1
9	7	9.3	557	(7	D97210	extracellular neut
7	76.5	٠	332	7	B90522	hypothetical prote
00	76.5	6.9	411	7	JC7869	cell wall-lutic be
σ,	76.5	6.9	768	7	B97725	outer membrane pro
10	75.5	9.5	245	Н	S74926	sensory transduct;
17	75.5	9.5	444	0	B64119	glucose-1-phosphat
12		9.1	448	7	C95257	choline binding pr
13	75	9.1	673	0	T48701	hypothetical profe
14	75	9.1	1013	Н	800801	Na+/K+-exchanging
15	~	٠	1013	N	C24639	Na+/K+-exchanging
16	73.5	8.9	613	7	A99552	olidoendopeptidase
17		٠	277	N	S17600	myelin proteolipid
18	73	8.8	277	N	151270	myelin proteolipid
19	73	•	870	N	827514	mosquitocidal toxi
20	72.5	8.	164	7	G96632	Ω
21	72.5	•	591	0	G90181	
22	72.5	•	768	7	D71726	
23	72.5	8.8	911	N	S70911	transferrin-bindin
24	. 72	8.7	616	~	A55796	ecarin precursor -
25	71.5	8.7	238	N	AG2396	two-component resp
56	71.5	8.7	303	(1	F86158	alternative splici
27	ч	8.7	640	Ŋ	B32935	hypothetical prote
28	71.5	8.7	929	N	T03473	acetate-CoA ligase
29	71	8.6	434	7	B81716	

glycosidase homolo outer membrane por	probable exported levanase homolog v	alpha, alpha-phosph	hypothetical prote	5-methyltetrahydro	hypothetical prote	site-specific DNA-	xylose isomerase (	XmnI methyltransfe	glucosvltransferas	hypothetical prote	qlutamine-fructose	acetyl-CoA synthet
AD1380 MMECPC	AI0442 E70035	H83758	S28277	AD1845	AD1963	JS0102	AE3425	JC4925	T30858	A96684	569793	H84206
21	0 0	00	1 73	0	7	н	~	~	7	~	~	7
1310	448 516	559	1139	1178	323	330	435	620	1577	162	604	929
8 8 6 7.	ໝ ໝໍໜ່	ໝ ໝໍແ	8.5	8.5	8.5	8.50	8 2	8.5	8.5	8.4	8.4	8.4
71,	70.5	70.5	70.5	70.5	70	70	70	70	70	69.5	69.5	69.5
30 31	32 33	3.4	36	37	38	33	40	41	42	43	44	45

# ALIGNMENTS

		Synechoc
		•
		protein
1 770	904	othetical

ocystis sp. (strain PCC 6803)

Cyspecies: Synechocystis sp.

AlVariety: PCC 6803 C.Date: 25-Apr-1997 #text\_change 20-Jun-2000

C, Accession: S76904

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystic

A; Reference number: \$74322; MUID: 97061201; PMID: 8905231

A.Accession: S76904
A.Status: preliminary
A.Molecule type: DNA
A.Rosidues: 1-474 <KRN>
A.Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18816.1; PID:g165396
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein slr0459

Query Match
Best Local Similarity 27.6%; Pred. No. 2;
Matches 32; Conservative 11; Mismatches 48; Indels 25; Gaps

9

413 42 KPGQEFPYYVYMIPKGTEYDDQR--W----ILESVGGDHYKLKNKFSGRYLVYGTFDYF 94 356 QPĠQTISYSLSKPLKGGEFASVTLVWERLVQLLDSNGNQQYDLGESFQAQPL--SNLDLF 엄 ò

95 LT--AGAA------VREMDHFKFTADGTGKYDISSKANG-----HPRSRGKNW 134 ò

В

RESULT 2

Cybecies: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Spacession: C98122
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F.
E, R.; Leellanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: C98122
A;Status: preliminary
A;Accession: C98124
A;Accession: C98144
A;

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C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                139 PNYRGRQY-LLEKGE 152
                                                                                                                                                                                                                                                                                                                                                                                     PRSRGKNWGVMKDGE 141
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A, Residues: 1-174 <CHA>
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286 RYFF 289
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C;Superfamily: chromatin remodelling complex ATPase chain ISWI; bromodomain homology
                                                                                                                   11;
                                                                                                                                                                                                                                                                                 57 GTEYDDQRWILESVGGDHYKLK---NKFSGRYLVYGTFDYFLTAGAAVREMDHFKFTADG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 DPESNKKRYLLKDANGKKRDLEGTTKRFEHLLSLSGLFKHFIESKAA--KDPKFRQVLDV 153
                                                                                                                                                                                               217 PGEKVHYDQIL-----EKDGYKWLSYTAYNGSYRYVQLEAVNKNPLGNSVLSSTGGTHYP 271
                                                                                                                                                                                                                                                    76 KLKANKFSGRYLVYGT-FDYFLTAGAA----VREMDHFK---FTA-DGTGKY----- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 QSFFVLTLAIFGAASDNPIADRK---CIVISDGDLVMHERKPGQEF-----PYYVYMIPK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 ENLFKIILAIF-----LQEKKKYDC--ISSGSIM----TASEEYLENLKPFQVGLPPH 95
                                                                                                                                                                -----ILESVGGDHY- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MyAlternate names: beta-s-crystallin
NyAlternate names: beta-s-crystallin
NyAlternate names: beta-s-crystallin
NyAlternate names: beta-s-crystallin
C;Species: Cyprinus carpio (common Carp)
C;Accession: 807146
R;Chang, T.; Chang, W.C.
A;Chang, T.; Chang, W.C.
A;Afference number: 807146; MUID:88000706; PMID:3307924
A;Accession: 807146
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNF2 protein homolog YBR245c - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein YBR1633
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 08-Sep-2002
C;Accession: S46122
R;Allinovic, G.; Pohl, F.M.; Pohl, T.M.
A;Reference to the Protein Sequence Database, August 1994
A;Reference number: S45906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Gaps
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                     332 QNYQNQSGNISSYGSNNSSTVGWKKINGSWYHFKSNGSKSTGWLKDGSSWYY 383
                                                                                                                                                                                                                                                                                                                                               118 -----DISS----KANG---HPRSRG-KNWGVMKDGEKHYF 145
                                                                                                                   74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.5%; Score 78; DB 2; Length 1143; Best Local Similarity 23.3%; Pred. No. 19; Matches 37; Conservative 34; Mismatches 56; Indels
                                                                     DB 2; Length 448;
                                                                                                                   38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : : | | : | : | | : | 154 LEE----NKANG--KGKGKHQDVRRRKTEHEEDAELLKE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 TGKYDISSKANGHPRSRGKNWGVMKDGEKHYFTVENCOE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: nucleus; transmembrane protein F;305-321/Domain: transmembrane #status predicted <TVM>
                                                                     9.5%; Score 78; DB 2
23.8%; Pred. No. 6.5;
tive 19; Mismatches
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A; Cross-references: EMBL:Z36114; MIPS: YBR245c
A; Experimental source: strain S288C
                                                                                                                                                                43 PGQEFPYYVYMIPKGTEYDDQRW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: SGD:S0000449
                                                                                                                   41; Conservative
                                                                Query Match
Best Local Similarity
Matches 41; Conserv
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                            A; Gene: cbpD
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    C, Genetics
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lysozyme (BC 3.2.1.17) [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: P98050
B;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Y. P.; Sun, P.M.; Winkler, M.B.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Retus: preliminary
A;Molecule type: DNA
A;Status: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
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Cipate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 02-Jun-2003
Cipate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 02-Jun-2003
Cipate: 15-Sep-2001 #sequence not consider the cipate of the cip
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 ----KNKFSGRYLVY-----GTFDYFLTAGAAVREMDHFKFTADGTGKYDISSKANGH 126
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A;Cross-references: EMBL:NZ6834; NID:g213051; PIDN:AAA49206.1; PID:g213052
C;Superfamily: beta-crystallin
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 IVISDGDLVMHERKPGQEFPYXVYMIPKGTEYDDQRW------ILESVGGDHYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Gaps
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Best Local Similarity 25.0%; Pred. No. 9.3;
Matches 31; Conservative 18; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                              Query Match
9.3%; Score 77; DB 2; Length 174;
Best Local Similarity 26.7%; Pred. No. 2.8;
Matches 36; Conservative 18; Mismatches 41; Indels
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A;Molecule type: DNA
A;Residues: 1-411 <ASA>
A;Cross-references: DDBJ:AB078775
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Best Local Similarity
Matches 35; Conserv
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             A; Accession: JC7869
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cell wall-lytic beta-1,3-glucan-hydrolase precursor, BglM - Bacillus circulans
C;Species: Bacillus circulans
C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 31-Mar-2003
C;Accession: JC7869; PC7199
R;Asano, T.; Taki, J.; Yamamoto, M.; Aono, R.
Bloosci. Biotechnol. Biochem. 66, 1246-1255, 2002
Biotechnol. Biotechnol and structural analysis of bglM gene coding for the fungal cell wall-ly A;Reference number: JC7869; MUID:22152179; PMID:12162545
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By0522

By0522

By0524

By0524

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By0524

By0524

By0524

C;Species: Mycoplasma pulmonis

B;Chambaud, I:; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;

Mycled. Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-557 «KUR»
A;Cross-references: GB:AE001437; PIDN:AAK80471.1; PID:g15025540; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2517
C;Superfamily: zinc metalloendopeptidase, neutral protease type (elastase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AL445566; PID:g14089495; PIDN:CAC13255.1; GSPDB:GN00153 A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                     336 IISTAHYGQSYDNAYWDGSQMVYGDGD-----GSEFTYFSGDLDVVGHELTHGVTQY 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----DHYKLKNKFSGRYLVYGTFDYFLTAGAAVREM 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 TANLAYEDQSGALNESMSDVFGVLIQTYDKYNVKN---GGNWAFSASDWVVGDGLFLNNT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 ILESVGGDHYKLKNKFSGRYLVYGTFDYFLTAGAAVREMDHFKFTADGTGKYDI----- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 KLARIN-------LILINGFÖPDDT-HIGLRSEDTFNDDLTGNKFDIVLANPP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LTLAIFGAASDNPIADRKC----IVISDGDLVMHERKPGQEFPYYVYMIPKGTEYDDQRW 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMVAILNPESDSSIYDPCCGTGGMFIQAKQYLQKNNLPTDELKIY-----GQEFQNQTW 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
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                                                                                                                                                                                                                                         % Match 9.3%; Score 77; DB 2; Length 557; Local Similarity 23.4%; Pred. No. 11; les 36; Conservative 18; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                   9 VLTLAIFGAASDNPIADRKCIVISDGDLVMHERKPGQEFPYY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 DH--FKFTADGTGKYDISSKANGHPRSRGKNWGV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 THRALRSLANPT-LYDQPDNMMNYVNTSDDNGGV 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 FNVKKWQTNDISGDPRFA---WGMPPEGNGNY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SSKANGHPRSRGKNWGVMKDGEKHY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKGTEYDDQRWIL-ESVGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-332 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: MYPU 0820
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: DNA
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A;Accession: PC7199
A;Molecule type: protein
A;Residues: 28-42;95-111;152-170 <AS2>
C;Comment: This protein that is a fungal cell wall-degrading enzyme, hydrolyzes beta-1;?
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rjogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rc Science 293, 2093-2098, 2001
A;fitle: McAnanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sensory transduction system regulatory protein sll0649 - Synechocystis sp. (strain PCC 6 Shlternate names: protein sll0649 C;Species: Synechocystis sp. 4;Varies: Synechocystis sp. 2;Decies: Synechocystis sp. 2;Decies: Synechocystis sp. 2;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C;Accession: S74926 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outer membrane protein omp1 [imported] - Rickettsia conorii (strain Malish 7)
                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 FILLNLAVGGNWPGSPNNSTPFPSQMLVDYVRVYQDTGASNVISDGIYTIASKASGKVMD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 YYVYMIPKG-----TEY--DDQRWILESVGGDHYKLKNKFSGRYLVYGTPDYFLTAGAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 FDYFLTA-----GAAVREMDHFKFTADGTGKYDISSKANG--HPRSRGKNWGVMKD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AE006914; PIDN: AAL02740.1; PID: 915619252; GSPDB: GN00173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GDLVMHERKPGQEFPYYVYMIPKGTEYDDQRWILLESVGGDHYKLKNKFSGRY---LVYGT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Rickettsia conorii
C.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C.Accession: B97725
                                                                                                                                                                                                                                                                                                                                                                                                                       VISDGDLVMHERKPGQEFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                               Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 768;
                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 VREMD-----HFKFTADGTGKYDISSKANG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 LOOWDDNGSNAQRWKIVDVĠĠĠYŸKLVŠKVSĠ 376
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9.3%; Score 76.5; DB
Best Local Similarity 23.1%; Pred. No. 17;
Matches 30; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                           9.3%; Score 76.5; DB ilarity 23.0%; Pred. No. 8.3; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   7 FFVLTLAIFG----AASDNPIADRKCI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Superfamily: protective surface antigen D-15
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74; Gaps

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C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Accession: T48701
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
Submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24541
A;Accession: T48701
A;Accession: T48701
A;Accession: prelimary
A;Actessive: prelimary
A;Actessive: prelimary
A;Actessive: Teferences: EMBL:AL353817; GSPDB:GN00112; NCSP:1A9.50
A;Accessive: Cormid contig 1A9; strain 74
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLKNKFSGRYLVYGT-FDYFLTAGAA----VREMDHFK---FTA-DGTGKY------ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 PGEKVHYDQIL-----EKDGYKWLSYTAYNGSYRYVQLEAVNKNPLGNSVLSSTGGTHYF 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 KTKSAIKTEPLVSATVIDYYYPGBKVHYDQILEKDGYKWLSYTAYNGSRRYIQLEGVTSS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 -----DISS----KANG---HPRSRG-KNWGVMKDGEKHYF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 QNYQNQSGNISSYGSHSSSTVGWKKINGSWYHFKSNGSKSTGWLKDGSSWYY 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 9.1%; Score 75; DB 2; Length 448 Local Similarity 23.8%; Pred. No. 13; les 41; Conservative 18; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein 1A9.50 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGOEFPYYVYMIPKGTBYDDORW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 168/1; 316/2; 382/1; 626/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SP2201
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: B64119
   o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                         A,Residues: 1-245 <KAN>
A;Cross-references: EMBL:D90902; GB:AB001339; NID:g1652027; FIDN:BAA16966.1; PID:g165204
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Accession: B64119
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J. Gocayne, J.D.; Scott, J.; Stirley, J.S.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fubramann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; WUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: mucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-444 <TIGR>
A;Cossidues: 1-444 <TIGR>
A;Cossidues: 1-444 <TIGR>
A;Cross-references: GB:UJ2815; GB:142023; NID:g1574818; PIDN:AAC23006.1; PID:g1574822;
C;Superfamily: glucose-1-phosphate adenylyltransferase
C;Keywords: glycogen/starch biosynchesis; nucleotidyltransferase
F;45/Shinding site: fructose-1.6-bisphosphate (Lys) #status predicted
F;120/Binding site: substrate (Lys) #status predicted
F;202/Binding site: substrate (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  choline binding protein D [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| : : || : : || |
38 CIVINDGETGLRIFQEQVPDLIVLDLMLPKLDGLEVCTRIRQQPGSKDPYILMLTAKGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --RKPGOEFPYYVYMIPKGTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 245;
                                                                                                                                                                                          A,Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: ompR protein; response regulator homology
C; Keywords: phosphoprotein; transcription regulation
F;14-125/Domain: response regulator homology <RRH>
F;62/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 MLMDHVNSGAKCTVGCIEV-----PRSEAHEFGVMAVNE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 REMDHFKFTADGT-GKYDISSKANGHPRSRGKNWGVMKDGE 141
                                                                                                                               A; Reference number: S74322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.2%; Score 75.5; D
Best Local Similarity 30.7%; Pred. No. 5.8;
Matches 27; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 ID--RIIGLŚTGAĎDÝLVK-PŘSPŘEĽV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 YDDQRWILESVGGDHYKLKNKFSGRYLV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 CIVISDG------DLVMHE----
                                                                                                                                                                                                                             A, Molecule type: DNA
                                                                                                                                                                 A; Accession: S74926
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                                                                                                                                                                                                                                                      40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                600 -----ASRPLDLFTFELDGEGK--VKGVENGALREEGRSNGGGSKEGRR 641
                                                                                                                                                                                                                                                                                                                                               95 LTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSRGK-NWGVMKDGEK 142
Query Match 9.1%; Score 75; DB 2; Length 673; Best Local Similarity 29.4%; Pred. No. 21; Matches 32; Conservative 9; Mismatches 28; Indels
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Na/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - rat
NiAlternate names: Na-/K+-transporting ATPase alpha(III) chain
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Unn-1988 #sequence revision 23-Apr-1993 #text_change 19-Apr-2002
C;Accession: C24639; S00514; \( \bar{B}27180; \) A60470
R;Shull, \( \bar{G}.E.; \) Greeb, \( \alpha.T.; \) Lingnet, \( \alpha.E. \) A.
Biochamistry 25, 8125-8132, 1986
A;Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit farecommoner. A30512; MUID:87128908; PMID:3028470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Molecule type: mRNA
A. Residues: 1-1013 < SHU>
A. Residues: 1-1013 < SHU>
A. Fross-references: EMBL:M14513; NID:g203030; PIDN:AAA40777.1; PID:g203031
A. Mole: in the authors' translation 405-Ser is shown after residue 409 and, consequentle R. Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohta, T.; J. Biochem. 102, 43-58, 1987
J. Biochem. 102, 43-58, 1987
A. Fritle: Primary structures of two types of alpha-subunit of rat brain Na(+), K(+)-ATPas A. Reference number: 800460; MUID:88032933; PMID:2822682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1,'NL',4-103,'R',105-113,'E',115-127,'G',129-148,'Q',150-151,'T',153-165,'D
A; Residues: 1,'NL',4-103,'R',105-113,'E',115-127,'G',129-148,'Q',150-151,'T',153-165,'D
A; Cross-references: EMBL:NZ8648; NID:g205633; PIDN:AA41672.1; PID:g205634
A; Note: the authors translated the codon CAG for residue 149 as Glu, GGC for residue 19
R; Hsu, Y.M.; Guidotti, G.
Biochemistry 28, 569-573, 1989
A; Title: Rat brain has the alpha3 form of the (Na+,K+)ATPase.
A; Reference number: A60470; MUID:89229049; PMID:2540801
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A;Residues: 117-132;586-595,'X',597-601 <HSU>
C;Comment: The alpha-3 form appears to be highly ouabain-inhibitable, as is alpha-2 but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: MRNA
A.Molecule type: MRNA
A.Molecule type: MRNA
A.Molecule type: 1-907, (C., 909-1013 < MRN)
A.Molecule type: MRNA
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F;366/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;498/Binding site: ATP (Lys) #status predicted
F;707,711,716/Active site: Asp, Asp, Lys #status predicted
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21.5%; Pred. No. 33;
ive 23; Mismatches
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Best Local Similarity
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                  Ayonominitor, A.A.; Nonaetyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Mealkov, A.W.; E. A.; Wording, E.D.; Marchinitor, A.A.; Nonaetyrskaya, G.S.; Broude, N.E.; Ushkarev, Y.A.; Mealkov, A.W.; E. A.; Wording, E.D.; M. A.; Wording, M. A.; Wording
R;Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Melkov, A.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AIFGAASDN-PIADR-----YVY 52
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F;366/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;498/Binding site: ATP (Lys) #status predicted
F;707,711,716/Active site: Asp, Asp, Lys #status predicted
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21.5%; Pred. No. 33;
tive 23; Mismatches 56; Indels
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Best Local Similarity 21.5'
Matches 48; Conservative
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87 -VYGTEDYELTAGAAVREMDHFKFTADG	541 RVLGFCHYYLPEEQFPKGFAF-DCDDVNFTTDNLCFVGLMSMIDPPRAAVPDAVGKCRSA 599	114TGKYDISSKANGHPRSRGKNWGVMKDGEKHYFTVBN 149		Search completed: September 9, 2004, 15:29:21 Job time : 42 secs
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

September 9, 2004, 15:15:29; Search time 23 Seconds (without alignments) 344.116 Million cell updates/sec Run on:

US-10-768-874-2 825 1 MSITQSFFVLTLAIFGAASD......NWGVWKDGEKHYFTVENCQE 152 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	ļΰ	P11001 streptococc		_	oryctolad	10		_	-	gallus g		arabidop						O68040 rhodobacter		P06996 escherichia	Q9zhd9 buchnera ap				Q56714 vibrio para			-		Q09057 neisseria m		ž tr	m
SUMMARIES		OI	SCAA CHICK	GTF1 STRDO	YB95_YEAST	CRBS_CYPCA	SCAA_RABIT	GLGC_HAEIN	A1A3_HUMAN	A1A3_RAT	PEPF_MYCPU	MYPR_CHICK	MYPR_POEGU	F825_ARATH	ECAR_ECHCA	NSF_ARATH	SFR1_ARATH	RF1_STAEP	APRN_ENTHI	ACSA_RHOCA	OMPD_SALTY		6PGD_BUCAP	INA1_CAEEL	MTH3_HAEAE		LMB2_VIBPA		RHP9_SCHPO	COMIDICDI	SCAA_RAT	TBB1_NEIMB	SYL_NEIMA		GLMS_PYRAB
		BB																		1										⊣,			-	-	-
		Match Length																			362	367	473	1139	330	441	275	603	778	185	698	711	910	480	597
οN	Query	Match	12.1	o.	9.5	9.3	9.3	9.5	6	9.1	დ ი	8.8	80	ω ω	8.7	8.7	8.7	8.7	8.7	8.7	٠		٠		ໝູ ເກົາ	•		•	•	œ ،	•	٠	٠	٠	•
		Score	99.5	82	78	77	76.5	75.5	75	75	73.5	73	73	72.5	72	72	71.5	71.5	71.5	71.5	71	70.5	70.5	70.5	0.70	0/	69.5	69.5	69.5	68.5	68.5	68.5	68.5	80 (	æ 9
	Result	No.	1	~	m	<b>4</b> 1	ល	9	7	ω (	on ¦	0,0	T	12	13	T 1	15	919	17	18	13	20	21	223	57	4, 1	25	26	27	20 0	N 10	90	37	3.0	33

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Q24298 drosophila	Q9r9n1 rhizobium m	P41343 mesembryant	Q8yil6 brucella me	O8cv38 brucella su	P41581 citrobacter	P41583 citrobacter	017967 caenorhabdi	015375 homo sapien	027874 methanobact	Ogixt2 neisseria m	P03306 f genome po
CADE DROME	LPSE RHIME	FENR MESCR	TRMU_BRUME	TRMU BRUSU	6PGD_CITAM	6PGD CITFR	PDI1 CAEEL	MOT6 HUMAN	SYG METTH	SYL_NEIMB	POLG FMDV1
н	Н	Н	Н	Н	1	н	Н	↤	Н	Н	1
1507	340	365	398	398	445	445	485	505	565	876	2333
8 6	8.2	8.2	8.5	8.2	8.2	8.5	8.2	8.2	8.2	8.2	8.7
89	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5
34	J.	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 LTAG----AAVREMDHFKFTADGTGKYDISSKANGHPRSR--GKNWGVMKDGEKHYFTV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 YYFYPLPDGAEYCDYTKHVAW-----GYCYYKLLAEFKAD--VLGCFHKCRKPCKMTEYQ 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 169:4271-4278(1987).
-!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

CIRSCPCLNWYRRCSCAYYPYPLPDGAEYCDYT -> TCDH

OFFRASFFASFPGMLQSPNSRACPRAMLIR (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MFB28;
MEDILINE=87308014; PubMed=3040686;
MEDILINE=87308014; PibMed=1040686;
Perretti J.J., Gilpin M.L., Russell R.R.B.;
"Nucleotide sequence of a glucosyltransferase gene from Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 LSAGYSRWPSAVSE-DWVFYMLSQQNKYNITSKRNGVAKVNIFFEEWNYKTNGESPAFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
dlucostransferase-1 precursor (EC 2.4.1.5) (GTF-I) (Dextransucrase) (Sucrose 6-glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                              TGREAMS; TIGRO0859; ENAC; 1.
PROSITE; PS01206; ASC; 1.
Ion transport; Sodium transport; Ionic channel; Transmembrane;
Glycoprotein; Ubl conjugation; Alternative splicing; Sodium channel.
CTTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.1%; Score 99.5; DB 1; Length 637; 31.7%; Pred. No. 0.032; ive 12; Mismatches 41; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 YYVYMIPKGTEYDDQ----RWILESVGGDHYKLKNKFSGRYLVYGTF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        streptococcus downei (Streptococcus sobrinus).
Bacteria, Pirmicutes, Lactobacillales, Streptococcase, Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (In isoform short).
/FIId=VSP 006197.
D -> EL TIN REF. 2).
Q -> R (IN REF. 2).
; 5D15E616373971DA CRC64;
                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTIG=VSP 006196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1597 AA.
                                                                          EMBL; U62902; AAB50550.1; -.
EMBL; U62903; AAB50551.1; -.
EMBL; U62904; AAB50552.1; -.
EMBL; U58475; AAB04954.1; ALT_INIT.
INTERPRO; IPRO04724; ENAC.
InterPro; IPRO04873; Na+channel_ASC.
Pfam; PF00858; ASC; 1.
PRINTS; PRO1078; AMINACHANNEL.
TIGREPAMS; TIGREO885; ENAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73236 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Conservative
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578
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571
637
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578
637 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sobrinus MFe28.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1317;
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DOMAIN
TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1030 ILGRGADYVLSDQASNKYLNVSDDKLFLPKTLLGQ-----VVESGIRFDGTGYVYNSS 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1083 ITGEKVIDSFITEAGNLYYFGODGYNV----TGAQNIKGSNYYFLANGAALRNIVY--TD 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VGGDHYKLKNKFSGRYLVYGTFDYFLTAGAAVREMDHFKFT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
           AGGREGATION OF BATTERIAL CELLS AND FOOD DEBRIS.
-!- CATALYTIC ACTIVITY: SUCTOSE + {(1,6)-alpha-D-glucosyl} (N) = D-fuctose + {(1,6)-alpha-D-glucosyl} (N+1).
-!- SUBCELLAULAR LOCATION: Secreted.
-!- MISCELLANBOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,5-LINKED GLUCOSE AND SOME 1,6-LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF GLUCANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 IFGAASDNPIADR---KCIVISDGDLVMHERKPGQEFPYYVYMIPKGTEYDDQRWILES-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1137 AGGONHYYGNDGKRYENGYQQFGNDSWRYFKNGVWALGLTTVDGHVQYFDKDGVQ 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 ADGTGKY---DISSKANGHPRSRGKNW----GVMK-----DGEKHYFTVENCQ 151
OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                         EMBL, M17391, AAC63063.1; -.
InterPro, IPR002479; CW_binding.
InterPro, IPR03318; Glyco hydro_70.
Pfam; PF01473; CW_binding_1; 16.
Pfam; PF0324; Glyco hydro 70; 1.
Transferase; Glycosyltransferase; Signal; Repeat; Dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical 131.1 kDa helicase in ALG7-ENP1 intergenic region.
YBR245C OR YBR1633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALITIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
1.25 A. 2 B, AND 5 AC REPEATS.
A REPEAT.
AC REPEAT.
                                                                                                                                              -i- SIMILARITY: Belongs to family 70 of glycosyl hydrolases.
-i- SIMILARITY: Contains 19 cell wall binding repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.9%; Score 82; DB 1; Length 1597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A REPEAT (INCOMPLETE).
fw; B9E86A200868798E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          GLUCOSYLTRANSFERASE-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
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rive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B REPEAT. AC REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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Best Local Similarity 22.93
Matches 40; Conservative
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P38144;
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SEQUENCE
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FROM N.A.
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                      SOLUTION TO THE STANT OF THE ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 DPESNKKRYLLKDANGKKFDLEGTTKRFEHLLSLGGFKHPIESKAA--KDPKFRQVLDV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 QSFFVLTLAIFGAASDNPIADRK---CIVISDGDLVMHERKPGQEF-----PYYVYMIPK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 ENLFKIILAIF-----LQEKKKYDC--ISSGSIM----TASEBYLENLKPFQVGLPPH 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Gaps
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01-ApR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Beta crystallin S (Gamma crystallin S).
Edyrinus carpio (Common carp).
Eukaryota; Metacoa; Chocata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                              Aljinovic G., Pohl F.M., Pohl T.M.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family. SNF2L subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00690; DEAH ATP HELICASE; FALSE NEG.
Hypothetical protein; Hydrolase; Helicase; Nuclear protein;
ATP-binding; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.5%; Score 78; DB 1; Length 1129; 23.3%; Pred. No. 8.2; ive 34; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 327 DEAH BOX.
1129 AA; 131101 MW; 2CF86BAF553E6695 CRC64;
                                                                               Aljinovic G., Pohl F.M., Pohl T.M., Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 LEB----NKANG--KGKGKHQDVRRKKTEHEEDABLLKE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 TGKYDISSKANGHPRSRGKNWGVMKDGEKHYFTVENCQE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, 236114; CAA85208.1; -.
PIR; $46122; $46122.
GermOnline; 138788; -.
$GD; $0000449; 15W1.
GO; $GO:0005634; C:mucleus; IPI.
GO; $GO:000538; P:chrcmatin modeling; IGI.
InterPro; IPR00140; DBAD.
InterPro; IPR001650; Helicase C.
InterPro; IPR001650; Helicase C.
InterPro; IPR001005; NNP DNA_Dinding.
Pfam; PF00176; SNP2 N; Pfam; PF00176; SNP2 N; C.
SWART; $M00490; HELICC; 1.
SWART; $M00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 23.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
SEQUENCE FROM N.A.
                                            STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRBS CYPCA
P10112;
                                                                                                                                                                                                                    REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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    RRPRESERVENTE SOLUTION OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 ----KNKFSGRYLVY-----GTFDYFLTAGAAVREMDHFKFTADGTGKYDISSKANGH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 QLYDKGDFTGQ--VYESTEDCPSVVDRFRT----REVHSCK-VLDGIWIF----YEH 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCAA RABIT STANDARD; PRT; 640 AA.

097741; QSN133;
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2014 (Rel. 43, Last annotation update)
4miloristive sensitive sodium channel alpha subunit (Epithelial Na+channel alpha subunit) (Alpha BNAC) (Nonvoltage-gated sodium channel lalpha subunit) (Alpha NACH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the vertebrate eye lens.
-!- DOMAIN: Has a two-domain beta-structure, folded into four very similar greek key motifs.
-!- SIMILARITY: Belongs to the beta/gamma-crystallin family.
-!- SIMILARITY: Contains 4 beta/gamma crystallin 'Greek key' domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 IVISDGDLVMHERKPGQEFPYYVYMIPKGTEYDDQRW------ILESVGGDHYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Gaps
                                                 "Cloning and sequencing of a carp beta s-crystallin cDNA.";
Biochim. Biophys. Acta 910:89-92(1987).
-!- FUNCTION: Crystallins are the dominant structural components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             æ. 4.
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Bukaryota, Metazoa, Chordata; Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BETA/GAMMA CRYSTALLIN 'GREEK KEY'
BETA/GAMMA CRYSTALLIN 'GREEK KEY'
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BETA/GAMMA CRYSTALLIN 'GREEK KEY'
BETA/GAMMA CRYSTALLIN 'GREEK KEY'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2E5DBA95453D2897 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] -
SRQUENCE FROM N.A.
Kudlacek O., Weisz E., Wiener H., Plass H.;
                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.3%; Score 77;
MEDLINE=88000706; PubMed=3307924;
Chang T., Chang W.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 PNYRGRQY-LLEKGE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 PRSRGKNWGVMKDGE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 26.78 tes 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
82
88
129
172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
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Velazquez H., Silva T.C., Andujar B., Uaffer A., Ortiz D.;

"The rabbit DCT does not express amiloride sensitive sodium channel.";

"The rabbit DCT does not express amiloride sensitive sodium channel.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

"I FUNCTION: Sodium permeable non-voltage-sensitive ion channel inhibited by the diuretic amiloride. Mediates the electrodiffusion of the luminal sodium (and water, which follows osmotically) through the applical membrane of epithelial cells. Controls the reabsorption of sodium in Kidney, colon, lung and sweat glands.

"I SUBJUIT: Heerestoternamer of two alpha, one beta and one gamma subunit. A delta subunit can replace the alpha subunit. Interacts

"I SUBJUITUAR LOCATION: Integral membrane protein."

"I SUBJUITUAR LOCATION: Integral membrane protein.

"I STURIBARITY: Belongs to the amiloride-sensitive sodium channel
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 YYVYMIPKGTEYDDQR----WILESVGGDHYKLKNKFSGRYLVYGTF-----DYF 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sodium transport; Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Score 76.5; DB 1; Length 640; 0.5%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Indels
"The rabbit epithelial sodium channel.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF -> TS (IN REF. 2).
TQ -> AE (IN REF. 2).
17C84C100F69E133 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ubl conjugation; Sodium channel.
1 65 CYIOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . ) (
N-LINKED (GLCNAC. . ) (
N-LINKED (GLCNAC. . ) (
N-LINKED (GLCNAC. . ) (
S -> P (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
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N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          463 LSAGYSRWPSVTSQDWVFQMLSLQNNYTVSNKRNG 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ132108; CAA10571.1; -.
EMBL; AP229025; AAF43680.1; -.
InterPro; IPR0014724; EnaC.
InterPro; IPR001873; Na+channel_ASC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373
72734 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS, PRO1078, AMINACHANNEL.
TIGREAMS, TIGRO0859; ENAC, 1.
PROSITE; PS01206; ASC, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.5%;
                                               SEQUENCE OF 81-435 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00858; ASC; 1.
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290
374
488
222
264
372
640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
DOMAIN
                                                                                                                                                                                                                                                                                                                                      family.
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DOMAIN
TRANSMEM
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CARBOHYD
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437 AA.

PRT;

STANDARD;

GLGC\_HABIN ID GLGC\_HABIN

RESULT 6

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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 QERGEFVDMLPARQQIDDSTWYRGTADAVYQNMAIIKNHYRPKYILILAGDHIYKQDYSV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.T., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP + alpha-D-glucose 1-phosphate = diphosphate + ADP-glucose.
-!- PATHWAY: Glycogen biosynthesis; first step.
-!- PATHWAY: Belongs to the bacterial/plant glucose-1-phosphate adenylyltransferase family.
                                                        10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucose-1-phosphate adenylyltransferase (BC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase)
                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBL_TaxID=727;
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or send an email to license@isb-sib.ch).
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InterPro, IPR005836, ADP Glu pyroP.
InterPro, IPR005835, NTP transferase.
Pfam: PF00483; NTP transferase.
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PIR; B64119; B64119.
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ID A1A3_HUWAN STANDARD; PF

B1537; Q16732; Q969K5;

DT 01-JAN-1990 (Rel. 13, Created)
                              01-NOV-1995 (Rel. 32, Created)
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                                                                                                                                                                                                                                                    Haemophilus influenzae.
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Best Local Similarity
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Richards R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Barat N.K.,
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A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
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Human and mouse oDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                           for the
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Sevaridov B.D., Monastyrskaya G.S., Broude N.E., Ushkarev Y.A.,
Melkov A.M., Smirnov Y.V., Malyshev I.V., Allikmets R.L.,
Kostina M.B., Dulubova I.E., Kiyatkin N.I., Grishin A.V.,
Mcyanov N.N., Ovchinnikov Y.A.,
"Family of human Na(+),K(+)-ATPase genes. Structure of the gene of
isoform alpha-III.";
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MEDLINE=88255304; PubMed=2838329;

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Melkov Y.A., Monastyrskaya G.S., Broude N.E., Ushkaryov Y.A.,

Melkov A.M., Smirnov Y.V., Malyshev I.V., Allikmets R.L.,

Kostina M.B., Dulubova T.E., Kiyatkin N.I., Grishin A.V.,

Modyanov N.N., Sverdlov E.D.;

Modyanov N.N., Sverdlov E.D.;

Family of human Na+, K+-ATPase genes. Structure of the gene for is

catalytic subunit (alpha III-form) and its relationship with

structural features of the protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87162481; PubMed=3030810; Ovchinnisvo Y.A., Monastyrskaya G.S., Broude N.E., Allikmets R.L., Ushkaryov Y.A., Monastyrskaya G.S., Broude N.E., Allikmets R.L., Dulubova I.B., Petrukhin K.E., Gryshin A.V., Sverdlov V.E., Kiyatkin N.I., Kostina M.B., Modyanov N.N., Sverdlov W.E., Feeff anily of human Na+, K+ATPase genes. A partial nucleotide sequence related to the alpha-subunit.";
                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                 chain (EC 3.6.3.9)
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28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
20dium/potessium-transporting ATPase alpha-3 of
(Sodium pump 3) (Na+/K+ ATPase 3) (Alpha(III)).
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A Sverdiov E.D., Monastyrskaya G.S., Broude N.E., Ushkaryov Y.A.,
Allikmets R.L., Melkov A.M., Smirnov Y.V., Malyshev I.V.,
Dulobova I.B., Petrukhin K.E., Grishin A.V., Kijakin N.V.,
Mostina M.B., Sverdiov V.E., Modyanov N.N., Ovchinnikov Y.A.,
The family of human Na+,K+-ATPase genes. No less than five genes
and/or pseudogenes related to the alpha-subunit.",
The family of human Na+,K+-ATPase genes. No less than five genes
and/or pseudogenes related to the alpha-subunit.",
The FBBS Lett. 217:275-278(1987).

-I- FUNCTION: This is the catalytic component of the active enzyme,
Which catalyzes the hydrolysis of ATP coupled with the exchange of
sodium and potassium ions across the plasma membrane. This action
creates the electrochemical gradient of sodium and potassium ions across the plasma membrane. This action
creates the energy for active transport of various nutrients.

C. GATALYTIC ACTIVITY: ATP + H(2) O + Na(+)(In) + K(+)(Out) = ADP +
phosphate + Na(+)(Out) + K(+)(In).

C. SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                             gamma.
SUBCELULAR LOCATION: Integral membrane protein.
SIMLIARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IIC.
 MEDLINE=87247232; PubMed=3036582;
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EMBL; M37436; AAA51798.1; JOINED
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EMBL; M37438; AAA51798.1; JOINED
EMBL; M37462; AAA51798.1; JOINED
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M37440; AAA51798.1; 0

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AAA52286.1; AAA52286.1;

SEQUENCE OF 243-434 FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                       Min; 16230; C:sodium/potassium-exchanging ATPase complex; TAS.

R GO; GO:0005391; F:sodium/potassium-exchanging ATPase activity; TAS.

R GO; GO:0006810; P:transport; TAS.

R InterPro; IPR001757; ATPase BL-E2.

InterPro; IPR004014; Cation_ATPase.

InterPro; IPR004014; Cation_ATPase_N.

InterPro; IPR004014; Cation_ATPase_N.

InterPro; IPR004014; Cation_ATPase_reg.

InterPro; IPR004014; Cation_ATPase_reg.

InterPro; IPR004014; Cation_ATPase_reg.

InterPro; IPR004014; Cation_ATPase_reg.

InterPro; IPR00534; Hydrolase.

InterPro; IPR00122; E1-E2_ATPase_reg.

IPR00102; Hydrolase; 1.

R Pfam; PR00122; Hydrolase; 1.

R Pfam; PR00101; CATATPASE.

IRR PRINTS; PR00111; NAKATPASE.

IRR PRINTS; PR00111; NAKATPASE.

IRR PRINTS; PR00114; ATPASE_LEZ_ATPASE.

IRR PRINTS; RR00119; ATPASE_LEZ_ATPASE.

IRR PRINTS; RR00119; ATPASE_LEZ_ATPASE.

IRR PROSITE; PS00154; ATPASE_LEZ_Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Sodium/potassīum Transport; Transmembrane; Phosphorylation;
Magnesium; Metal-binding; ATP-binding; Multigene family.
DOMAIN
1 77 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 AIFGAASDN-PIADR------KCIVISDGDL-VMHER-KPGQEFPY----YVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 MIPKGTEYDDQRWILESVGGDH------YKLKNKFSGRYL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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; Pred. No. 14;
23; Mismatches
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                                                                                                  EMBL; M27570; AAA58380.1; JOINED.
EMBL; M27573; AAA58380.1; JOINED.
EMBL; BC009282; AAH09282.1; --
EMBL; BC009394; AAH05394.1; --
EMBL; BC015566; AAH15566.1; --
                                 AAA52286.1; JOINED.
AAA58380.1; -.
M28291; AAA52286.1; JOINED
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HSSP, P04191, 1EUL.
Genew, HGNC:801, ATPIA3.
MIM, 182350, -.
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121
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834
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929
                                     M28292;
M27577;
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                                 EMBL;
EMBL;
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MEDLINE=8747222; PubMed=3036582;
MEDLINE=87247222; PubMed=3036582;
Sverdlov E.D., Monastyrskaya G.S., Broude N.E., Ushkaryov Y.A.,
Allikmets R.L., Melkov A.M., Girinov Y.V., Malyshev I.V.,
Allikmets R.L., Melkov A.M., Grishin A.V., Kijatkin N.I.,
Mulobova I.E., Petrukhin K.E., Grishin A.V., Kijatkin N.I.,
Kostina M.B., Sverdlov V.E., Modyanov N.N., Ovchinnikov Y.A.;
The family of human Na+, K--Argase genes. No less than five genes
and/or pseudogenes related to the alpha-subunit.";
FRBS Lett. 217:275-78(1987).
The FRBS Lett. 217:275-78(1987).
C. !- FUNCTION: This is the catalytic component of the active enzyme,
which catalyzes the hydrolysis of ATP coupled with the exchange of
sodium and potassium ions across the plasma membrane. This action
creates the electrochemical gradient of sodium and potassium ions
creates the electrochemical gradient of various mutrients.

Droviding the energy for active transport of various mutrients.

C. !- CATALYTIC ACTIVITY: ATP + H(2)0 + Na(+)(In) + K(+)(out) = ADP +
phosphate + Na(+)(out) + K(+)(In).

C. !- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IIC.
                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB-Brain;
MEDLINE-88032933; PubMed=2822682;
MEDLINE-88032933; PubMed=2822682;
Hara Y., Urayama O., Kawakami K., Nojima H., Nagamune H., Kojima T.,
Ohta T., Nagano K., Nakao M.;
"Primary structures of two types of alpha-subunit of rat brain
Ma+.K+,-ATPase deduced from cDNA sequences.";
J. Biochem. 102:43-58(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Three differentially expressed Na, K-ATPase alpha subunit isoforms:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-87128908; PubMed=3028470;
Shull G.E., Greeb J., Lingrel J.B.;
"Molecular cloning of three distinct forms of the Na+,K+-ATPase
alpha-subunit from rat brain.";
                            PO6687; Q16732; Q9Z1G6; Oreated)
01-JAN-1988 (Rel. 06, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-NAR-2004 (Rel. 43, Last annotation update)
Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9)
(Sodium pump 3) (Na+/K+ ATPase 3) (Alpha(III)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herrera V.L.M., Emanuel J.R., Ruiz-Opazo N., Levenson R.,
PRT; 1013 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structural and functional implications."; J. Cell Biol. 105:1855-1865(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain, and Liver;
MEDLINE=88033255; PubMed=2822726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 25:8125-8132(1986).
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STANDARD;
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421 AVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRERNKKVAEIPFNSTNKYQL 480
                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last annotation update) Oligoendopeptidase F homolog (EC 3.4.24.-). PRFF ON MYPU 3210.
                                                               87 -VYGTFDYFL----TAGAAVREMDHFKFTADG--
                                                                                                                                                                      613 AA
                                                                                                                                                                                         (Rel. 40, Created)
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          NCBI_TaxID=2107;
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RILCETPO: IPRO00609; Cation_ATPASE.

RILCETPO: IPRO00609; Cation_ATPASE.

RILCETPO: IPRO006250; R1-E2_ATPASE_N.

RILCETPO: IPRO008250; R1-E2_ATPASE_N.

RILCETPO: IPRO008250; R1-E2_ATPASE_N.

RILCETPO: IPRO00894; Hydrolase.

RILCETPO: IPRO00899; Cation_ATPASE_N.

REAM; PRO00609; Cation_ATPASE_N; 1.

REAM; PRO0019; CATAPPASE.

DR PRINTS; PRO0112; R1-E2_ATPASE_N; 1.

REAM; PRO0119; CATAPPASE.

DR RINTS; PRO0119; CATAPPASE.

DR TIGRAMS; TIGRO1106; ATPASE_IE2; 1.

ROSITE; PSO0124; ATPASE_IE2; 1.

RW MAGINESIUM; Metal-binding; ATP-binding; Multigene family.

CUTOOLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY PKA) (BY SIMILARITY)
BINDING OF PHOSPHOINOSITIDE-3 KINASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.1%; Score 75; DB 1; Length 1013; 21.5%; Pred. No. 14; .ive 23; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAD -> MUL (IN REF. 3).

A -> R (IN REF. 3).

A -> G (IN REF. 3).

A -> G (IN REF. 3).

E -> Q (IN REF. 3).

E -> D (IN REF. 3).

C -> T (IN REF. 3).

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E -> D (IN REF. 3).

MISSING (IN REF. 3).

I -> V (IN REF. 3).

MISSING (IN REF. 3).
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CYTOPLASMIC (POTENTIAL)
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C -> F (IN REF. 1).
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LUMENAL (POTENTIAL).
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V -> K (IN REF. 3)
M27577; AAA58380.1; -. M27570; AAA58380.1; JOINED. M27573; AAA58380.1; JOINED.
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1013 AA; 111691 MW;
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Best Local Similarity 21.5%,
Local 48; Conservative
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BMBL; AL45564; CACL.

Rypulist; MYPU 3210; -.

B Mypulist; MYPU 3210; -.

B Mypulist; MYPU 3210; -.

B Mypulist; MYPU 3210; -.

B ROSITE; PS00142; ZINC PROTESE; M3: 1.

B ROSITE; PS00142; ZINC PROTESE; ZINC (CATALYTIC) (BY SIMILARITY).

METAL 395 395 ZINC (CATALYTIC) (BY SIMILARITY).

A99 399 ZINC (CATALYTIC) (BY SIMILARITY).

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A09 310 ZINC (CATALYTIC) (BY SIMILARITY).

A01 ZINC (CATALYTIC) (BY SIMILARITY).

A09 210 ZINC (CATALYTIC) (BY SIMILARITY).

A09 210 ZINC (CATALYTIC) (BY SIMILARITY).

A09 310 ZINC (CATALYTIC) (BY SIMILARITY).

A09 310 ZINC (CATALYTIC) (BY SIMILARITY).

A01 31; 27; Gaps SGRYLVYGT------FDYFLTAGAAV-REMDH--FKFTADGTGKYDISS 121 SGAYSIGSTHGIDKKFILMNFDGTLNSVSTLSHEMGHSMHSYFSDKTQPQSLSS 416 STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.; "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153 (2001).
--- COPACTOR: Binds 1 zinc ion (By similarity).
--- SIMILARITY: Belongs to peptidase family M3. Mycoplasma pulmonis. Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma. 114 -----TGKYDISSKANGHPRSRGKNWGVMKDGEKHYFTVEN 149 600 GIKVIMVIGDHPITAKA-----IAKGVGIISEGNE---TVED 633 82 363 셤 ð 9 ⋩

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36 HEALIGIEQLIETYF---SKNYQDYEYLIDVI------HAFQYVIYGTASFFFLYG 82
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                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIG1. Chem. Hoppe-Seyler 372:865-874(1991).

-!- FUNCTION: THIS IS THE MAJOR MYELIN PROTEIN FROM THE CENTRAL
NERVOUS SYSTEM. IT PLAYS AN IMPORTANT ROLE IN THE FORMATION OR
MAINTENANCE OF THE MULTILAMELLAR STRUCTURE OF MYELIN.

-!- SUBGELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: Belongs to the myelin proteolipid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00575; WYELIN PLP_1; 1.

Myelin; Transmembrane; Structural protein; Lipoprotein; Palmitate.

INIT_MST

1 9 CYTOPLASMIC (POTENTIAL).

TRANSMEM 1 36 1 (POTENTIAL).

DOMAIN 36 58 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schliess F., Stoffel W.; "Evolution of the myelin integral membrane proteins of the central
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                III (FOIENIIAL):
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
S-palmitoryl cysteine (By s:
BY SIMILARITY.
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                                                                                                                                                                        01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Puplin proteolipid protein (PLP) (Lipophilin)
PLP1 OR PLP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                II (POTENTIAL).
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                                                                                                                           276 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92126243; PubMed=1722981;
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PIR; S17600; S17600.
InterPro; IPR001614; Myelin PLP.
PRO1275; Myelin PLP; T.
PRINTS; PR00214; MYELINPLP.
SWART; SM00002; PLP; 1.
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                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken)
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276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system."
Biol. Chem. Hoppe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                           MYPR CHICK P23289;
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S-palmitoyl cysteine (By similarity).

S-palmitoyl cysteine (By similarity).

S-palmitoyl cysteine (By similarity).

"Imitoyl cysteine (By similarity).
"Osteine (By similarity).
"Osteine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campagnoni C.W., Kampf K., Mason B., Handley V.W., Campagnoni A.T., "Isolation and characterization of a cDNA encoding the zebra finch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myelin proteolipid protein.";
Neurochem. Res. 19:1061-1065(1994).
Neurochem. Res. 19:1061-1065(1994).
-!- FUNCTICN: THEIS IS THE MAJOR MYELIN PROTEIN FROM THE CENTRAL
NERVOUS SYSTEM. IT PLAYS AN IMPORTANT ROLE IN THE FORMATION OR
MAINTERANCE OF THE MULTILAMELLAR STRUCTURE OF MYELIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the myelin proteolipid protein family.
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PROSITE; P800575; MYBLIN PLP_1; 1.
PROSITE; P801004; MYBLIN PLP_2; 1.
Myelin; Transmembrane; Structural protein; Lipoprotein; Palmitate.
INIT MET

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                     Poephila guttata (Zebra finch) (Taeniopygia guttata).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
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99 A-----AVREM-DHFKFTADGTGKYDISSKANGHPRSRG 131
                                  II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
III (POTENTIAL).
EXTRACELIULAR (POTENTIAL).
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S-palmitoyl cysteine (i
BY SIMILARITY.
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10-OCT-2003 (Rel. 42, Last annotation update)
Myelin proteolipid protein (PLP) (Lipophilin).
                                                                                                                                                                                                                  276 AA
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Pred. No.
                                                                                                                                                                                                                  PRT;
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InterPro: IPROO1664; Myelin_PLP.
Pfam; PF01275; Myelin_PLP; T.
PRINTS; PR00214; MXELINPLP.
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                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=59729;
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28; Gaps

25; Conservative

Matches

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S.
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White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E. Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conm L., Conway A.B., Cromay A.R., Creasy T.H., Dewar K.,
Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
A dill J.B., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,
Kim C.J., Koo H.L., Kremenetskaia I., Khartz D.B., Kwan A., Lan B.,
Langin-Hooper S., Lee A., Luros J.S., Maiti R., Marziali A.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Lin X., Liu S.X., Luros J.S., Maiti R., Marziali A.,
Langin-Hooper S., Lee A., Luros J.S., Maiti R., Marziali A.,
Langin-Hooper S., Lee A., Luros J.S., Maiti R., Marziali A.,
Langin-Hooper S., Lee A., Luros J.S., Maiti R., Marziali A.B.,
Langin-Hooper S., Lee A., Luros J.S., Maiti R., Marziali A.,
Langin-Hooper S., Los C., Schwartz J.R., Shinn P., Southwick A.M.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
T. "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DISS 121
                                               98
                                                                   36 HEALTCTEQLIETYF---SKNYQDXEFLIDVIHG------PQYFIYGTAAFFFLYG 82
                                      39 HERKPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKLKNKFSGRYLVYGTFDYFLTAG
                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 164;
                                                                                                                                                     99 A------AVREM-DHFKFTADGTGKYDISSKANGHPRSRG 131
    36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 GDHYKLKNKFSGRYLVYGTFDYFLTA--GAAVREMDHFKFTADGTGKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 408:816-820(2000).
-!- SIMILARITY: Belongs to the peroxiredoxin 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSEP; P30044; 1H40.
InterPro; IPR000866; AhpC-TSA.
Pfam; PR0578; AhpC-TSA; 1.
Hypothetical protein.
SEQUENCE 164 AA; 17841 MW; 8D934C52C7311E84 CRC64;
                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATIG60740 OR F8A5.25.
    15; Mismatches
                                                                                                                                                                                                                                                                                    164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.8%; Score 72.5;
27.8%; Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AC002292; AAB71961.1; -. PIR; G96632; G96632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; Conservative
26; Conservative
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thaliana.";
                                                                                                                                                                                                                                                                               F825 ARATH 022711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                         F825_ARATH
Matches
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GKAEELKSKGIDEIICFSVNDPFVMKAWGKTYQENKHVKFVADGSGEYTHLLGLELDLKD 122

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                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Venom gland,
MEDLINE=95151760; PubWed=7849037;
MEDLINE=95151760; PubWed=7849037;
Mishids S., Fujita T., Kohno N., Atoda H., Morita T., Takeya H.,
Kido I., Paine M.J.I., Kawabata S.-I., Iwanaga S.;
"CDNA cloning and deduced amino acid sequence of prothrombin activator
(ecarin) from Kenyan Echis carinatus venom.";
Biochemistry 34:1771-1778 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE-75260130; PubMed-956136;
Morita T., Iwanaga S., Suzuki T.;
"The mechanism of activation of bovine prothrombin by an activator
isolated from Echis carinatus venom and characterization of the new
                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Ĉraniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Viperinae, Echis.
NCBI_TaxID=40353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metalloproteinase activity.
-!- COFACTOR: Binds 1 zinc ion and 1 calcium ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: Catalyzes the conversion of prothrombin to alphathrombin through formation of a thrombin intermediate. Has
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 191-228; 353-357; 372-383; 393-415; 446-453; 459-474; 553-561; 574-597 AND 610-616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBUNIT: Monomer.
-!- SIMILARITY: Belongs to peptidase family M12B.
-!- SIMILARITY: Contains 1 disintegrin domain.
                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last sequence update)
10-0cr-2003 (Rel. 42, Last annotation update)
Edrin precursor (EC 3.4.24.).
Echis carinatus (Saw-scaled viper).
                     123 KGLG---IRSRRFALLLDNLK--VTVANVE 147
                                                                                                                                616 AA
122 KANGHPRSRGKNWGVMKDGEKHYFTVENCQ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom, PD000664; Disintegrin; 1.
SMART, SM00608; ACR; 1.
SWART, SM00050; DISIN; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001590; PeptIdase_M12B.
InterPro; IPR00280; PeptIdase_M12B.
Pfam; PF00200; disintegrin; 1.
Pfam; PF01562; Pep M12B propep; 1.
Pfam; PF01421; Reprojysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006586; ADAM cysteine.
InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            active intermediates.";
J. Biochem. 79:1089-1108(1976).
                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D32212; BAA06910.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00289; DISINTEGRIN
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A55796; A55796.
HSSP; P18619; 1FVL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; M12.151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity)
                                                                                                                            BCAR BCHCA
090495;
                                                                                                            ECAR_ECHCA
                                                                                        RESULT 13
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Mayer K.F.X., Schweller C., Wambutt R., Murphy G., Volckaert G., Poll T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M. de Simone V., Obermaier B., Mache R., Mueller M., Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., Reichert B., Porterfelle D., Perez-Alonso M., Boutry M., Bancroft I., A Reichert B., Porterfelle D., Perez-Alonso M., Boutry M., Bancroft I., Langham S.-A., McCullagh B., Bilham I., Robben J., Vandenbussche F., Langham S.-A., McCullagh B., Bilham I., Robben J., Vandenbussche F., Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor B., Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Holzer B., Brandt A., Peters S., van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., A Berneiser S., Hempel S., Feldgausch M., Lamberth S., Van den Daele H., De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 YDDQRWILESVGGDHYKL---KNK--FSGRY--LVYGTFDYFLTAGAAVREMDHFKF--- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 YEDAMQYEFEVKGEPVVLHLEKNKELFSEDYSETHYSSDDREITTNPSVE--DHCYYHGR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 VLTLAIF---GAASDNPIADRKCIVISDGDLVMHERKPGQEFPYYVYMIPKGT----E 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 IICLAVEPYQGCS------IILGSGNVNDYE----VVYPQKVTALPKGAVQQPEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9NOY8; Q9ZPH6; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-MAR-2004 (Rel. 43, Last sequence update) Vesicle-fusing ArPase (EC 3.6.4.6) (Vesicular-fusion protein NSF) (N-ethylmalelimide sensitive fusion protein) NSF) (N-NSF) OR Art4604910 OR TiJ1.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eddicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 ---TADGTGKYDISSKANGHPRSRGKNWGV----MKDGEKH----YFTVENCQE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                8.7%; Score 72; DB 1; Length 616; 24.1%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                     26; Mismatches 60; Indels
                                                                                                                                                                                                       (PROBABLE).
PROSITE; PS50214; DISINTEGRIN 2; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Metal-binding; Calcium;
Prothrombin activator; Zymogen; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                               (PROBABLE)
                                                                                                                                                                                                                                                                                                                                               09CC3CD1AD252346 CRC64;
                                                                                                                                                                        CALCIUM (BY SIMILARITY).
                                                                                                                                                                                         CALCIUM (BY SIMILARITY)
ZINC (CATALYTIC) (PROBA
                                                                                                                         METALLOPROTEINASE-LIKE.
                                                                                                                                      DISINTEGRIN-LIKE.
                                                                                                                                                                                                                           (CATALYTIC)
(CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     742 AA.
                                                                                                                                                          CYS-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                           ZINC
                                                                                                                                                                                                                                                                                                                                                 69462 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                           3341
2219
2261
3261
497
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   616 AA;
                                                                                                                                                                                                                                                              219
261
295
326
497
                                                                                       2204
201
201
201
201
337
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CARBOHYD
                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
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DOMAIN
DOMAIN
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CHAIN
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NSF_ARATH
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RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
Retett A., Rajandream M.A., Lyne M., Benes Y., Rechmann S.,
Borkova D., Bloecker H., Scharfe M., Grimm M., Lochnert T.-H.
Borse S., de Haan M., Fartmann B., Granderath K., Danner D., Herzl A.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Panner D., Herzl A.,
RA Gabel C., Fuchs M., Partmann B., Granderath K., Panner D., Herzl A.,
RA Gabel C., Fuchs W., Fartmann B., Granderath K., Panner B.,
RA Gabel C., Hiller R., Schmidt W., Lecharny A., Paubourg S.,
A Chefdor F., Cober R., Berger C., Monfort A., Tacon J., Torres A.,
RA Chefdor F., Coke R., Berger C., Monfort A., Tacon J., Jorres A.,
RA Perz-Perz A., Purnelle B., Bent B., Johnson B., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Accaria P., Bevan M., Wilson R.K., Mewes H.-W., Stocker S., Bielke C.,
RA Actoneking T., Kallcki J., Schutz K., Huang E., Spiegel L.,
RA Schoneking T., Kallcki J., Graves T., Harmon G., Badwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Mersen J., Spieth J., Ryan E., Jones K., Drone K., Cotton M., Joshu C.,
RA Marca M.J., Berghoff A., Jones K., Drone K., Cotton M., Johnson A.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Waby I.K., O'Shaughnessy A., Hameed A., Lodhi M., Johnson A.,
RA Granat S., Shodky N., Hassegawa A., Hameed A., Lodhi M., Johnson A.,
RA Granat S., Shodky N., Hassegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martiensen R., Wocombie W.R.,
RA Sharra M.A., Martiensen R., Wocombie W.R.,
RA Hallana W.A., Martiensen R., Wolling R., Challand R., Lodhi M., Andrian J., R.,
Ra Hallan M. A., Martiensen R., Wolling R., Challand R., C STRAIN=CV. Columbia,

MEDLINE=22254850; PubMed=14593172;

MEDLINE=22254850; PubMed=14593172;

MEDLINE=22254850; PubMed=14593172;

MEDLINE=22254850; PubMed=14593172;

MEDLINE=22254850; PubMed=14593172;

MI WI H.C., Kim C.J., Nguyen M., Pahm P.K., Cheuk R.F.,

Rarlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

M. Arakawa T., Pann G.C., Dondera C.S., Deng J.M., Akiyama K., Ansari Y.,

Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Briu A., Goldsmith A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hauan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Saki M., Sakurai T.,

Satou M., Tamse R., Vayaberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis Science 302:842-846(2003).

-!- FUNCTION: Involved in vesicle-mediated transport. The ATPase activity of NSF serves to disassemble the SNARE complex, freeing the components for subsequent pairing and fusion events.

-!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.

-!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.

-!- SUBJUNIT: Hexamer. Binds to SNARE-SNAP complexes to form 20S particles (By similarity).

-!- SUBJUNITHAR LOGATION: Cytoplasmic (By similarity).

-!- SIMILARITY: Belongs to the AAA ATPase family.

-!- CAUTION: Ref.1 sequences differ from that shown due to erroneous Nature 402:769-777(1999). SEQUENCE FROM N.A. 

gene model prediction.

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EMBL; AL161502; CAB81033.1; ALT SEQ. EMBL; AF128393; AAD17345.1; ALT SEQ. EMBL; AX102111; AAM26681.1; -.

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SEQUENCE FROM N.A.

STRAIN=CV. Columbia;

Whistolnes-21016719; Pubmed=11130712;

Whistolnes-21016719; Pubmed=11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

R. Theologis A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

R. Buchler B., Chan L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

R. Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

R. Chung W.K., Conn L., Conway A.B., Fong B., Fujii C.Y.,

R. Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

R. Hutter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

R. Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

R. Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

R. Lin X., Liu S.X., Liu Z.A., Luros J.S., Malti R., Marziali A.,

R. Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
                                                                                                                                                                                                                                                                                                                                            54 FILSLCGHGSIRDGNIALNAIQRRHARVSTGDMVSVSRFVPPENFDLAMLTLELEFVKKG 113
                                                                                                                                                                                                                                                                                                                8 FVLTLAIFGAASDNPIA----DRKCIVISDGDLVMHER-KPGQEFPYYVY-----MIPKG 57
                                                                                                                                                                                                                                                                                                                                                                      58 TEYDDORWILESVGGDHYKLKNKFSGRYLVYG---TFD----YFLTAGAA-VREMDH 106
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=95372342; PubMed=7644475;

Lazar G., Schaal T., Maniatis T., Goodman H.M.;

"Identification of a plant serine-arginine-rich protein similar to the mammalian splicing factor SF2/ASF.";

Proc. Natl. Acad. Sci. U.S.A. 92:7672-767(1995).
                                                                                                                                                                                                                                                                                            24; Gaps
     A HOSEPTO, IPRO03593, AAA ATPRASE.
R INTERPRO; IPRO03593, AAA ATPRASE.
R INTERPRO; IPRO03959, AAA ATPRASE.
R INTERPRO; IPRO03959, AAA STPASE.
R INTERPRO; IPRO03910; AAA STPASE.
R INTERPRO; IPRO04010; AAA, SU.
R INTERPRO; IPRO0401, Cdc48_2, R.
R Fam; PPO2933; cdc48_2; I.
R Ffam; PPO2933; cdc48_1, I.
R Pfam; PPO2933; cdc48_N; I.
R PFAM; PRO0382; AAA; 2.
R ROSITE; PSO0674; AAA; 1.
R TYANSPORT; Protein transport; Hydrolase; Endoplasmic reticulum; Golgi stack; ATP-binding; Metal-binding; Magnesium; Repeat.
W Golgi stack; ATP-binding; Metal-binding; Magnesium; Repeat.
T NP_BIND 537 544 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERIL ARATH STANDARD; PRT; 303 AA.

022315; 022314; 023201;
15-DEC-1998 (Rel. 37, Last sequence update)
11-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 37, Last sequence update)
Pre-mRNA splicing factor SF2 (SR1 protein).
SF2 OR AT1602840 OR F22D16.16 OR F22D16.30.
Arabidopsis thaliana (Wouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; NTBLTAXID=3702;
                                                                                                                                                                                                                                                           8.7%; Score 72; DB 1; Length 742; 28.8%; Pred. No. 20; ive 16; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
Su C.-L., Schuler M.A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                   544 544 MAGNESIUM.
742 AA; 81487 MW; 39611058DEAC4A32 CRC64;
                                                                                                                                                                                                                                          SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Enropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 DLVMHERKPGQEFPYYYYMIPKGTE-----YDDQRWILESVGGDHYKLKNKFSGRYLV 87
                                                                                                                                                                                           -i- FUNCTION: Can promote splice site selection in vitro presumably by antagonizing the effects of the Al heterogeneous nuclear ribonucloprotein. May have an essential function during early
Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoid=022315-2; Sequence=VSP_005859, VSP_005860;
TISSUE SPECIFICITY: Ubiquitous.
PTM: Extensively phosphorylated on serine residues in the RS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the splicing factor SR family.
-!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 YGTFDYFLTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234
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                                                                                                                                                                                                                                                                     plant development.
SUBCELLULAR LOCATION: Nuclear (Potential).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.7%; Score 71.5; Di
25.2%; Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Name=1; Synonyms=SF2A;
IsoId=O22315-1; Sequence=Displayed;
Name=2; Synonyms=SF2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
SMART: SM00360; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, M98340; AAA32856.1; -.
EMBL, AF001035; AAB71385.1; -.
EMBL, AF001035; AAB71386.1; -.
EMBL, AC009525; AAF02881.1; -.
                                                                                                                                                                         Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.2*
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; F86158; F86158.
PIR; S71185; S71185.
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                                                                                                                                                  thaliana.";
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; ;

Search completed: September 9, 2004, 15:28:36 Job time : 26 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 9, 2004, 15:25:00 ; Search time 120 Seconds (without alignments) 399.656 Million cell updates/sec Run on:

US-10-768-874-2 825 1 MSITQSFFVLTLAIFGAASD......NWGVMKDGEKHYFTVENCQE 152 Title: Perfect score: Sequence:

Scoring table:

1017041 seqs, 315518202 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*
sp\_nmammal:\*
sp\_mammal:\*
sp\_organelle:\*
sp\_phage:\*
sp\_phage:\* sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* SPTREMBL 25:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	.v. miilimis 607700	085047 moraxella c	O7xmd8 orvza sativ	O8a9r8 bacteroides	P74698 synechocyst	Ogttfl canis famil	Ogttf2 canis famil	091bg9 arthrobacte	O8dmz4 streptococc	0924i8 streptococc	08dp07 streptococc	097g52 clostridium	O98rc7 mycoplasma	Oakkh3 bacillus ci	O7v8p5 prochloroco	Q92j67 rickettsia
SUMMARIES	ΩI	002700	085047	Q7XMD8	Q8A9R8	P74698	Q9TTF1	Q9TTF2	Q9LBQ9	OBDMZ4	Q9Z4J8	Q8DP07	Q97G52	Q98RC7	O8 KKH3	Q7V8P5	Q92J67
	DB	5	N	10	16	16	9	9	N	16	7		16		7	16	16
	% Query Match Length DB	152	712	868	389	474	280	329	1048	448	501	501	557	332	411	422	768
٥	Query Match	100.0	10.7	10.2	10.1	10.1	8.6	9.8	9.6	9.5	9.3	ю. Э	6.9	9.3	9.3	9.3	9.3
	Score	825	88	84	83.5	83.5	80.5	80.5	79.5	78	77	77	77	76.5	76.5	76.5	76.5
	Result No.	1	61	ო	4	ស	9	7	œ	თ	10	11	12	13	14	15	16

O8irz5 phthorimaea	Ogaht7 streptococc			~	Q84b46 gamma-prote	09kgz2 streptococc					Q95mj0 tupaia qlis		P96948 neisseria m				Q9exu2 klebsiella	098187 acrocephalu	Q986g7 rhizobium l	Q95p16 trypanosoma	Q8xsg4 ralstonia s	Н	Q9s3x9 klebsiella	Q8ktd6 alcaliqenes	Q88y38 lactobacill	082ip3 streptomyce	Q8ie04 plasmodium	
12 Q8JRZ5	2 Q9AHT7	16 Q8NZ52	16 P72948	O	2 Q84B46			16 Q8K5M1			6 Q95MJ0			2 P70745	_	_			16 Q986G7	5 Q95PL6	9	2 Q8G9Q2		2 QBKTD6		16 Q82IP3	5 QBIE04	2 Q03988
185	492	676	245	153						1053				1051					342	350		2835		276		572		870
9.2	•	9.5	•	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	0.6	0.6	0.6	0.0	0.6	9.0	9.0	8 6.	8.0	8 6.	9.0	8.8	8.8	•	•	8.8	8 8
76	76	92	75.5	75	75	75	75	75	75	75	~	74.5	74.5	74.5	74	74	74	74	73.5	73.5	73.5	73.5	73	73	73	73	73	73
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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NCBI_TaxID=818;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 YLVYG----TFDY---FLTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSRGKNWGV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 NDEYGHSSEFTVDFSKKSLTGGLFSNLQDHHKGKVTKTKRYDINARIHGN-RFRGSATAI 377
                                                                                                                                                                                                                                       STRAINE 3,

XREALINE 98380363; PubMed = 9712766;

XA MEDLINE = 98380363; PubMed = 9712766;

XA Myers L.E., Yang Y.D., Du R.D., Wang Q., Harkness R.E.,

RA Schryvers A.B., Xlein M.H., Loosmore S.M.;

RT bactericidal antibodies and is a potential vaccine antigen.";

RT Dactericidal antibodies and is a potential vaccine antigen.";

RM Infect. Immun. 66:4183-4182 (1998).

DR QO; GO:0016020; C:membrane; IEA.

DR QO; GO:0016020; C:membrane; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR HOROSTE; PRO000437; Prok_lipoprot S.

DR InterPro; IPR000437; Prok_lipoprot S.

DR Pfam; PF01298; Lipoprotein 5; 1.

DR Pfam; PF01298; Lipoprotein 5; 1.

SO SEQUENCE 712 AA; 76863 MW; C50808DD11AF2C09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 MHERKPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKL.------KNKFSGR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y., Yu Z., Chen L., Ran D.L., Weng Q.J., Zhang L., Zhang L., Zhu Y., Liu Y., Liu Y., Lu Y., Zhang Y.J., Lu Y., Liu Y., Lu Y., Zhang Y.J., Lu Y., Lu Y., Zhang Y.J., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Zhang R.Q., Cau J.P., Fu G., Wang S.Y., Zhang X.X., Shao C.Y., Sun Y.Y., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzee, Oryza.
                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Moraxella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
10.7%; Score 88; DB 2; Length 712;
Best Local Similarity 27.8%; Pred. No. 3.2;
Matches 37; Conservative 10; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
0SJNBa0061020.21 protein.
                                                                                             01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) reansferrin binding protein B.
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                                                       712 AA
                                                                                    Created)
                                                       PRT;
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                                                                       085047;
01-NOV-1998 (TrEMBLrel. 08,
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                                                       PRELIMINARY;
                                                                                                                                                           Moraxella catarrhalis.
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
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01-OCT-2003
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                                                       085047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 ODYQHGAGTM-YYHNGDLYVGNWANDKREGEGTYTWANGAKYSGHWKNDKKNGKGTMNWD 189
                                                                                                                                                                                                                                                                                                                                       80 KFSGRYLVYGTFDYPLTAGAAVRE----MDHFKFTADGTGKYD-----ISSKANGHP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 VISDGDLVWHERKPGQEFPYYVYMIPKGTEYDDQRWILESVGGD---HYKLKNKFSGRYL 86
                                                                                                                                                                                                                                                                                                     -----KLKN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.Y., Gordon J.I.;
Agenomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Gaps
                                                                                                                                                                                                                                              40; Gaps
Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AL662974; CAE04665.1; -. SED067842B4EB651 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.1%; Score 83.5; DB 16; Length 389; Best Local Similarity 24.4%; Pred. No. 4.2; Matches 33; Conservative 20; Mismatches 59; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                              Query Match 10.2%; Score 84; DB 10; Length 868; Best Local Similarity 24.8%; Pred. No. 11; Matches 33; Conservative 20; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase; Complete protecome.
SEQUENCE 389 AA; 44241 MW; CE805074D37E851B CRC64;
                                                                                                                                                                                                                                                                                                        43 PGQEFPYYVYMIPKGTEYDDQRWIL-----ESVGGDHY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative phosphatidylinositol-4-phosphate 5-kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE016929, AA075854.1; -. 60, 60, 60, 0016301; F.kinase activity, IEA. InterPro; IPR003409; MORN. PF02493; MORN; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TrEMBLrel. 02, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 -----GVMKDGEKH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 DGCKYDGDWKDDVRH 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 -RSRGKN---WGV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 GRTRGKGVIPWKI 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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1 MSITOSFFVLTLAIFGAA------SDNPIADRKCIVISDGD-LVMH 39
            7 MELNNILFVWTLLLYGAASMKSQAYFNKTGELPCHFTNSQNISLDELVVFWQDQDKLVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20093996; PubMed=10630300;
Yang S., Sim G.-K.;
"New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=142;
Tomita R., Tonozuka T., Sakano Y.;
"Molecular cloning of the Glucodextranase gene from Arthrobacter globiformis 142, and Expression in Escherichia coli.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AB033333; BAB20416.1; -.
GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
GO; GO:0005976; P:polysaccharide metabolism; IEA.
                                                                                                                              67 ELYRGKENPONVHRKYKGRISFDKDNWILRL----HNIQIKDKGLY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.8%; Score 80.5; DB 6; Length 329; 27.1%; Pred. No. 6.9; ive 13; Mismatches 38; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Micrococcaceae; Arthrobacter. NCBI_TaxID=1665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 ERKPGQEFPYYVYMIPKG-TEYDDQRWILESVGGDHYKLKNKFSGRY 85
                                                                     40 ERKPGQEFPYYVYMIPKG-TEYDDQRWILESVGGDHYKLKNKFSGRY
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SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS500290; IG_MHC; 1.
SRQUENCE 329 AA; 37774 WW; D98BB63437BF7B73 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                   329 AA.
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                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenetics 50:349-353(1999)

EMBL, AF106826, AAF17297.1; -.

HASP, P33681, IDR9.

InterPro; IPR007110; Ig-11ke.

InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Conservative
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                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       B7-2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 QPGQTISYSLSKPLKGGEFASVTLVWERLVQLLDSNGNQQYDLGESFQAQPL--SNLDLF 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SDNPIADRKCIVISDGD-LVMH 39
                                                                                                                                                                                                                                                                   MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu B., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 KPGQEFPYYVYMIPKGTEYDDQR--W----ILESVGGDHYKLKNKFSGRYLVYGTFDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 ITDOGGATPVVCSSOSKVDNVEHFLCPIASTGKYTIQVKHQGGGTAPRPENYALSW 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 LT--AGAA-----VREMDHFKFTADGTGKYDISSKANG-----HPRSRGKNW 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-20093996; PubMed=10630300;
Yang S., Sim G.-K.;
"New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Indels
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HSSP; P33681; 1DR9;
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-WHC.
InterPro; IPR003596; Ig-W.
SWART; SW00406; IG-IX; 1.
PROSITE; PS002290; IG-IXE; 1.
PROSITE; PS002290; IG-IXE; 1.
SRQUENCE 280 AA; 32265 MW; 3C8EBCA4D826A7F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D90917; BAA18816.1; -.
PIR; S76904; S76904.
Hypothetical protein; Complete proteome.
SEQUENCE 474 AA; 52308 MW; D8553459649716E8 CRC64;
                                                                                                                                                    Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein slr0459.
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Last annotation update)
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                                                                                                                        Synechocystis sp. (strain PCC 6803)
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 27.6
Matches 32; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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QSTTF1

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à g RESULT 6
09TTF1
AC 09TTF1
DT 01-M
RX MEDL
RX M

Matches

4

27; Gaps

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SEQUENCE FROM N.A.
MEDLINE=21429245; PubMed=11544234;
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                                                                                                                                                                                                                                                     PRELIMINARY;
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NCBI_TaxID=171101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus.
                                                                                                                                                                                                                                                                                                                          01-MAY-1999
01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                 396 FPQTSRVDGTIGONGIQLDETAFPİLLANQİGRTDAGFYRNELKPAAD-----YLVAAGP 450
                                                                                                                                                                                                                                                                                                                                                                                                      59 EYDDQRWILESVGGDHYKL-------KNFSGRYLVYGTFDYFLTAGAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                            451 KTPQERW--EETGG--YSTSTLASQIAALAAADIAGKMGDAGSAAVYRA-----TADEW 501
                                                                                                                                                                                                                                                                                                   8 FVLTLAIFGAASDN------PIADRKCIVISDGDLVMHERKPGQEFPYYVYMIPKGT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 PGEKVHYDQIL----EKDGYKWLSYTAYNGSYRYVQLEAVNKNPLGNSVLSSTGGTHYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21429245; PubMed=11544234;
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S.,
Hoskins J., Alborn W.E. Jr., Funder D.J., Fuller W., Geringer C.,
Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Genome of the bacterium Streptococcus pneumoniae strain R6.";
                                                                                                                                                                                                        DB 2; Length 1048;
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                                                                                                                                                                                                                                                     60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                        1048 AA; 109140 MW; 09D4D124B478DF4F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 VREMDHFKFTAD --- GTGKYDISSKANGHPRSRG-KNWG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 QRSTEKWMFTTNGPVGDGKYYLRISATGNPNDGATRDWG 540
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Choline binding protein D.
                                                                                                                                                                                                                                                     16; Mismatches
                                                                                                                                                                                                     9.6%; Score 79.5; I
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InterPro; IPR006425; Glucan glucosid.
InterPro; IPR000165; Glyco hydro 15.
InterPro; IPR008928; Glyco_trans_6hp.
Pfam; PP00723; Glyco_hydro 15; 1.
TIGRFAMS, TIGR01535; Glucan glucosid; 1.
PROSITE; PS00820; GluCOAMYIASE; 1.
SEQUENCE 1048 AA; 109140 MW; 09D4D12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 183:5709-5717(2001).
EMBL; AE008565; AAL00808.1; -.
PIR; C98122; C98122.
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InterPro; IPR002479; CW binding.
InterPro; IPR003646; SH3_bac.
Pfam; PP05257; CHAP; 1.
Pfam; PP01473; CW binding_1; 3.
SMART; SM00287; SH3b; 2.
PROSITE; PS50911; CHAP; 1.
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                                                                                                                                                                                                                                                     38; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 -----YLTGSGAMATDEVIMDGARYIFAASGELK------EKKDLNVGW-VHRDGK 285
272 KIKSAIKTEPLVSATVIDYYYPGEKVHYDQILEKDGYKWLSYTAYNGSRRXIQLEGVTSS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99340545; PubMed=10411730;
Garcia P., Gonzalez M.P., Garcia E., Garcia J.L., Lopez R.;
The molecular characterization of the first autolytic lysozyme of Streptococcus pneumoniae reveals evolutionary mobile domains.";
Mol. Microbiol. 33:128-138(1999).
BMBL, ANORGOS, CARARRES.1;
GO, GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
GO, GO:0003796; F:rarbohydrate metabolism; IEA.
InterPro; IPR002479; CW binding.
Fram; PF01473; CW binding.1; 5.
Glycosidase; Hydrolase; Signal.
                                                                                                               118 -----DISS-----KANG---HPRSRG-KNWGVMKDGEKHYF 145
                                                                                                                                                      332 QNYQNQSGNISSYGSNNSSTVGWKKINGSWYHFKSNGSKSTGWLKDGSSWYY 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.3%; Score 77; DB 2; Length 501; Best Local Similarity 25.0%; Pred. No. 27; Matches 31; Conservative 18; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 1,4-BETA-N-ACETYLMURAMIDASE.
58682 MW; A6774B6DBF2EB704 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-NAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
,4-beta-N-acetylmuramidase precursor (BC 3.2.1.17)
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LYTC OR SPR1431.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 GDLVMHERKPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKLK-----NKFSGRYL 86
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkoultz B.J., Lu J., Matsshima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R., Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3%; Score 77; DB 16; Length 501;
25.0%; Pred. No. 27;
Live 18; Mismatches 43; Indels 32; Gaps
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MEDLINE-2135325; Dubmed-11/0/;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Glisson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm D., Soucaille P., Daly M.J.,
Bennett G.N., Koonin B.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Glostridium acetobutylicum.";
J. Bacterium Glostridium acetobutylicum.";
J. Bacterium Clostridium acetobutylicum.";
Part. A60152; A60152.
PIR: D97210; D97210.
                                                                                                                                                                                                                                                                                                           GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA. GO; GO:0003796; F:lysozyme activity; IEA. GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridium.
Clostridium.
                                                                                                                                                                                       Glass J.I.;
"Genome of the bacterium Streptococcus pneumoniae strain R6.";
"Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
BMBL; AB008513; AAL00235.1;
PIR; F98050; F98050.
                                                                                                                                                                                                                                                                                                                                                                             Interpro; IRR002479; CW binding.
Pfam; PR01473; CW binding 1; 5.
Glycosidase; Hydrolase; Complete proteome.
SEQUENCE 501 AA; 58681 MW; A2D74FC911241DA4 CRC64;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Extracellular neutral metalloprotease, NPRE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Conservative
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Matches 31; Conserv
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RYFF 289
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AC 097G52
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DT 011-0C
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Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Noszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Dalanchard A.,
The complete genome sequence of the murine respiratory pathogen
The complete genome sequence of the murine respiratory pathogen
The complete genome sequence of the murine respiratory pathogen
The complete genome sequence of the murine respiratory pathogen
The Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
BRMBL; AL45563; CAC13255.1; -.
BRMBL; B90522; B90522.
BRMPL; B90522; B90522.
BRMPL; B90522; B90520; -.
BRMBL; AL45563; CAC13255.1; -.
BRMBL; AL45563; CAC13255.1; -.
BRMBL; AL45563; CAC13255.1; -.
BRMBL; AL45563; CAC13255.1; -.
BRMBL; AL45563; CAC13255.1; -.
BRMBL; AL45563; CAC13255.1; -.
BRMBL; AL45563; CAC13255.1; -.
BRMBL; AL45564; FINA binding; IEA.
GO; GO:000670; F:SIA-seperate activity; IEA.
GO; GO:0006306; F:DNA methylation; IEA.
TALANCAL THE ACT AND AMODIFICATION; IEA.
THE ACT AND AMODIFICATION; IEA.
THE ACT AND AMODIFICATION; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        336 IISTAHYGOSYDNAYWDGSQMYYGDGD-----GSEFTYFSGDLDVVGHELTHGVTQY 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 PKGTEYDDQRWIL-ESVGG-----DHYKLKNKFSGRYLVYGTFDYFLTAGAAVREM 104
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                                                                                                                                                                                                                                                  9.3%; Score 77; DB 16; Length 557; 23.4%; Pred. No. 32; tive 18; Mismatches 62; Indels
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Restriction-modification enzyme subunit M3 (EC 2.1.1.72)
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Pfam; PF01447; Peptidase_M4; 1.
Pfam; PF0286; Peptidase_M4; 1.
Pfam; PF03413; Pep M4, propep; 1.
PRINTS; PR00730; THERMOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Proctase; Metalloprotease; Complete proteome.
SEQUENCE 557 AA; 60362 NW; DBBB1854F499669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 VLTLAIFGAASDNPIADRKCIVISDGDLVMHERKPGQEFPYY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 THRALRSLANPT-LYDQPDNMNNYVNTSDDNGGV 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.3%; Score 76.5; 1
23.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003665; Methylase M. InterPro; IPR002295; NIZNG mifrase. InterPro; IPR003365; NG DNA Mtase. InterPro; IPR002052; NG MAESE.
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                                                                                                                                                                                                                                                                                                             36; Conservative
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Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2107;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 YYVYMIPKG-----TEY--DDQRWILESVGGDHYKLKNKFSGRYLVYGTFDYFLTAGAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                        66 ILESVGGDHYKLKNKFSGRYLVYGTFDYFLTAGAAVREMDHFKFTADGTGKYDI----- 119
                                                                                                                ---LILNGFDPDDT-HLGLRSEDTFNDDLTGNKKFDIVLANPP 102
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BABI, AB078775; BAGG195.1; -

PIR, JC7869; JC7869.

GO; GO:0004555; F: hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.

GO; GO:0004577; F: hydrolase activity; IEA.

GO; GO:000577; F: hydrolase activity; IEA.

GO; GO:000577; F: hydrolase activity; IEA.

InterPro; IPR00895; Ricing like.

InterPro; IPR00897; Ricing like.

InterPro; IPR0077; Ricing like.

InterPro; IPR0077; Ricing like.

Fam; PF0072; Ricing like.

PEam; PF0072; Ricing like.

PEam; PF0072; Ricing like.

PEam; PF0072; Ricing like.

PEam; PF0072; Ricing like.
4 LAVAILNPESDSSIYDPCCGTGGMFIQAKQYLQKNNLPTDELKIY-----GQEFQNQTW 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asano T., Taki J., Yamamoto M., Aono R.; "Cloning and structural analysis of bglM gene coding for fungal cellwall-lytic b-1,3-glucan-hydrolase BglM of Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                           OBKKH3;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1,3-(1,3,1,4)-beta-D-glucan 3(4)-glucanohydrolase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 AA; 45341 MW; 4587D730188D312D CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.3%; Score 76.5; DB 2;
23.0%; Pred. No. 24;
tive 23; Mismatches 59;
                                                                                                                                                                     120 -----SSKANGHPRSRGKNWGVMKDGEKHY 144
                                                                                                                                                                                                      103 FNVKKWQTNDISGDPRFA---WGMPPEGNGNY 131
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                                                                                                                                                                                                                                                                                                                                                                            411 AA.
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PROSITE; PS50231; RICIN_B_LECTIN; 1.
Signal; Hydrolase.
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Les 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                58 KLARIN---
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Q8KKH3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                              "Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation.",
                                                                                                                                                                                          MEDLINE=22825698; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 AA; 47864 MW; DA22A25063A33E74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.3%; Score 76.5; DB Best Local Similarity 32.1%; Pred. No. 25; Matches 26; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 9, 2004, 15:31:28
Job time : 123 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 424:1042-1047(2003).
EMBL; BX572095; CAE20465.1; -.
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome
                                                                                                  NCBI_TaxID=74547;
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

9, 2004, 15:14:53 September Run on:

3; Search time 122 Seconds (without alignments) 352.026 Million cell updates/sec

US-10-768-874-2 Title: Perfect score:

1 MSITQSFFVLTLAIFGAASD......NWGVMKDGEKHYFTVENCQE 152 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* geneseqp1980s:\* geneseqp1990s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

#### SUMMARIES

% Query e Match Length DB ID	5 100.0 152 2 AAW74589 Simulium	10.7 722 2 AAY43379 Aav43379	10.2 1297 7 ADC94925 B.	9.8 280 2 AAY41078 Aav41078 Can	9.8 329 2 AAY41076 Aav41076	9.6 1047 3 AAB35740 Aab35740	9.5 1129 6 ABR52906 Abr52906	9.3 332 7 ADC23977 Adc23977	9.3 448 3 AAY71551 Aay71551	6 9.2 471 2 AAW61216 Aaw61216	6 9.2 471 5 ABP54635 Abp54635	6 9.2 471 7 ADC45239 S.	9.2 490 3 AAY81745 Str	9.2 506 6 ABU02034 Abu02034	9.2 179 3 AAG38201 Are	9.2 180 3 AAG10251 Aag10251	9.1 446 5 AAU76561	9.1 446	9.1 448 3	9.1 448 6 ABU02732 Abu02732	9.1 676 5 ABP29594 Str	9.1 676 6 ABU46865 · Abu46865	5 9.1 1013 7 ADB85134 Adb85134	
% Query Match Lengt	0.00		01	ω.	8.	9.	.5	e.	۳.	2.	7.	.2	۲,	.2	e.	.2							Н	
Score	825	88	84.5	4 80.5	80.5	79.5	7 78	8 76.5		10 76	7	7			75	75.	17 75				1 75		23 75	

Ade57724 Rat Prote	Ade55707 Human Pro	Ade57720 Rat Prote	Ade55706 Rat Prote	Ade55703 Rat Prote	Abp77467 N. gonorr	Pr	Aaw52304 Glucodext	Abb08211 Escherich	Abb98574 Dextran s	Abr55594 Amino aci	Aar14529 Mosquitot	Aar41020 Insectici	Aar75410 B. sphaer	Aag10253 Arabidops	Aag32193 Arabidops	Aag38203 Arabidops	Aag38202 Arabidops		Aag32192 Arabidops	
7 ADES7724	7 ADE55707	7 ADE57720	7 ADE55706	7 ADE55703	6 ABP77467	6 ABU37086	2 AAW52304	5 ABB08211	5 ABB98574	6 ABR55594	2 AAR14529	2 AAR41020	2 AAR75410	3 AAG10253	3 AAG32193	3 AAG38203	3 AAG38202	3 AAG10252	3 AAG32192	
1013	1013	1013	1014	1014	837	878	1051	367	2835	2835	870	870	870	110	110	110	162	162	164	
9.1	9.1	9.1	9.1	9.1	0.6	0.6	0.6	6.8	6.8	8.9	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.8	
75	75	75	75	75	74.5	74.5	74.5	73.5	73.5	73.5	73	73	73	72.5	72.5	72.5	72.5	72.5	72.5	
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

#### ALIGNMENTS

Blood-feeding black fly; salivary gland erythema protein; SVEP; vasodilative activity; wound healing; suppression; immune response; treatment; peripheral resistance; atherosclerosis; heart failure; hypertension; graft rejection; autoimmune disease. Simulium vittatum salivary gland erythema protein (SVEP). AAW74589 standard; protein; 152 AA. (revised)
(first entry) 25-MAR-2003 09-DEC-1998 AAW74589; RESULT 1 AAW74589 

WO9840089-A1

Simulium vittatum.

98WO-US004795 12-MAR-1998; 17-SEP-1998.

97US-0040418P. 98US-00036355. 13-MAR-1997; 06-MAR-1998;

(AUBU ) UNIV AUBURN. (UYAR-) UNIV ARIZONA.

Swaim SF; Cupp EW, Cupp MS, Ribeiro JMC,

WPI; 1998-506475/43.

N-PSDB; AAV54348

New isolated vasodilative protein from salivary glands of Simulium species - useful, e.g. for regulating blood pressure or promoting wound healing and as immunomodulator.

Claim 5; Page 18; 27pp; English.

fly) salivary gland erythems procein (SVEP). The proteins exhibit vasodilative activity and wound healing promoting properties, as well as the capacity to suppress certain immune responses in a mammal. The vasodilative or immunomodulating proteins from the salivary glands of simulium species may be administered to a mammal in order to treat peripheral resistance or to modulate the immune response. The proteins The present sequence represents Simulium vittatum (blood-feeding black

may be coupled to

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Nucleic acid encoding transferrin binding protein 2 of Moraxella catarrhalis, useful for diagnostics, immunization and recombinant protein
                                                                                                                                                                                                                                                                                                                                      61 DDQRWILLESVGGDHYKLKNKFSGRYLVYGTFDYFLTAGAAVREMDHFKFTADGTGKYDIS 120
                                                                                                                                                                                                                                                                                                                                                                         61 DDQRWILESVGGDHYKLKNKFSGRYLVYGTFDYFLTAGAAVREMDHFKFTADGTGKYDIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the Moraxella catarrhalis strain 3 transferrin binding protein (TDp2) of the invention. The DNA sequence is also referred to as the TDpB gene. The TDpB gene is used to produce recombinant TDp2; for identification or diagnosis of Moraxella, or for cloning related species, using hybridisation assays; and for genetic immunisation against woraxella infections, e.g. octitis media. The TDp2 proteins are useful as antigens, either in vaccines (including components of conjugate vaccines that contain antigens from other bacteria or from tumours, in which case
                 failure, hypertension, peripheral resistance, stenoses and in particular peripheral vasodilation. These proteins may also be used to suppress the immune system, to inhibit or prevent the development of antibodies or cellular immunity to a protein, treat graft rejection and autoimmune diseases. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TbpB gene; Tbp2; transferrin binding protein; diagnosis; otitis media; genetic immunisation; Moraxella infection; antigen; vaccine; detection; antitumour antibody production; therapy.
                                                                                                                                                                                                                                                                                               1 MSITQSFFVLTLAIFGAASDNPIADRKCIVISDGDLVMHERKPGQEFPYYVYMIPKGTEY
                                                                                                                                                                                                                                                              1 MSITQSFFVLTLAIFGAASDNPIADRKCIVISDGDLVMHERKPGQEFPYYVYMIPKGTBY
                                                                                                                                                                                                                         Gaps
 can also be used for treating atherosclerosis of extremities, heart
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                                                                                                                                                                                      Length 152;
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                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harkness RE, Loosmore SM,
                                                                                                                                                                                  100.0%; Score 825; DB 2;
100.0%; Pred. No. 8.1e-87;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                              SKANGHPRSRGKNWGVMKDGEKHYFTVENCQE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SKANGHPRSRGKNWGVMKDGEKHYFTVENCQE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catarrhalis strain 3 tbp2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY43379 standard; protein; 722 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Fig 4; 114pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schryvers AB,
                                                                                                                                                                                                                       Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-620376/53
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ31947
                                                                                                                                                 Seguence 152 AA;
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Klein MH;
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                                                                                                                                                                                    Query Match
                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                       85 YLVYG-----TFDY---FLTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSRGKNWGV 136
                                                                                                                                                                                                                                                                                                               329 NDEYGHSSEFTVDFSKKSLTGGLFSNLQDHHKGKVTKTKRYDINARIHGN-RFRGSATAI 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regularcry element, a cell comprising the vector and single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract
                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an
                                                                                                                                                                                                             ----KNKFSGR
they elicit production of antitumour antibodies that may be coupled to chemotherapeutic agents or biologically active agents) or to raise antibodies (for use a diagnostic reagents and for treating Moraxella infections), also for detecting Moraxella antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid derived from Enterococcus faecium encoding Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                         42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                                                                                                               Query Match 10.7%; Score 88; DB 2; Length 722; Best Local Similarity 27.8%; Pred. No. 0.81; Matches 37; Conservative 10; Mismatches 44; Indels
                                                                                                                                                                                                               38 MHERKPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 4552; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. faecium protein sequence SEQ ID 4552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC94925 standard; protein; 1297 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                       388 NKDNESKAKHPFT 400
                                                                                                                                                                                                                                                                                                                                                                   137 MKDGE---KHYFT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecium.
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N-PSDB; ADC91271.
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                                                                                               Sequence 722 AA;
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Sequence 280 AA;

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The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritic and atogic diseases such as atogic dermatitis. They can be used in mammals such humans, dogs, catts, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                       infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans - derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faccium infections. The present sequence represents one if the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- VYGTFDYFLTAGAAVREMDHFKFTADGT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 VIVDGEKVIHPIGEPDSFVYKDSEETTNYAEYKIIESQNPEGFKEPDENDTWILRLYDNA 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease; allergic reaction; infectious disease; tumor development; canine; graft rejection; inflammation; arthritis; atopic dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 VISDGDLVMHE-----RKPGQEFPYYV-YMI-----PKGTEYDDQR--WIL----ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated B7 and CTLA4 nucleic acids, used to develop products for
endocarditis, wounds and abdominal-pelvic
                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                          10.2%; Score 84.5; DB 7; Length 1297; 28.8%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY41078 standard; protein; 280 AA.
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98US-00062597.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 VGGDHYKLKNKFSGRYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               36; Conservative
   bacteraemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canine B7-2S protein.
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                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 GKYDI 119
                                                                                                                                                                                                                                                             Sequence 1297 AA;
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AAY41078

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88888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : | | : | | : | | : | | | HELNNILLFVWTLLLLYGAASMKSQAYFNKTGELPCHFTNSQNISLDELVVFWQDQDDKLVLY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SDNPIADRKCIVISDGD-LVMH 39
                                                              --SDNPIADRKCIVISDGD-LVMH 39
                                                                                         7 MELINNILFVMTLLLYGAASMKSQAYFNKTGELPCHFTNSQNISLDELVVFWQDQDKLVLY 66
                                                                                                                                                                                                                                                                                                                                            B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease; allergic reaction; infectious disease; tumor development; canine; graft rejection; inflammation; arthritis; atopic dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated B7 and CTLA4 nucleic acids, used to develop products for
                                    Gaps
                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 329;
                                                                                                                                          Indels
                                    Indels
                                                                                                                          40 ERKPGOEFPYYVYMIPKG-TEYDDORWILESVGGDHYKLKNKFSGRY
         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.8%; Score 80.5; DB 2;
27.1%; Pred. No. 2;
                                    38;
         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating, e.g. autoimmune and atopic diseases.
9.8%; scc... 27.1%; Pred. No. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSITQSFFVLTLAIFGAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 97-99; 148pp; English
                                                                                                                                                                                                                                AAY41076 standard; protein; 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US006187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0078765P.
98US-00062597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.18;
                                                                   1 MSITQSFFVLTLAIFGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ27913, AAZ27915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Conservative
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-571822/48.
                                                                                                                                                                                                                                                                                                                  Canine B7-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                      Local Similarity
ses 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                        W09947558-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-1998;
                                                                                                                                                                                                                                                                                       20-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                             AAY41076;
          Query Match
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                           Best Loc
Matches
                                                                                                                                                                                                 RESULT 5
                                                                                                                                                                                                                  AAY41076
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RESULT AAB357

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The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent prevention of a disease or disorder. Note: The sequence data for this prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the Buropean Patent Office. The complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 GTEYDDQRWILESVGGDHYKLK---NKFSGRYLVYGTFDYFLTAGAAVREMDHFKFTADG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 DPESNKKRYLLKDANGKKFDLEGTTKRFEHLLSLSGLFKHFIESKAA--KDPKFRQVLDV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 ENLFKIIIAIF-----LQEKKKYDC--ISSGSIM----TASEEYLENLKPPQVGLPPH 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme; nitrilase; nitrile; cyanobyrdin; ammonia; biocatalyst; enantiomer; chiral medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 677; 17pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein sequence (SeqID 244) exhibiting nitrilase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 QSFFVLTLAIFGAASDNPIADRK---CIVISDGDLVMHERKPGQEF--
                            Multiprotein complex, eukaryote, drug target, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 TGKYDISSKANGHPRSRGKNWGVMKDGEKHYFTVENCQE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 LEE----NKANG--KGKGKHQDVRRKKTEHEEDAELLKE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 78; DB 6
23.3%; Pred. No. 21;
tive 34; Mismatches
                                                                                                                                                                                                                                                                                                                          vin A, Grandi P, Krause R, Ki
Schultz JD, Superti-Furga GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC23977 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is available on CD-ROM
                                                                                                                                                                                                20-DEC-2001; 2001EP-00130253
                                                                                                                                                                                                                                       15-MAY-2001; 2001EP-00111774
                                                                     Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-250078/25.
                                                                                                                                                                                                                                                                              (CELL-) CELLZOME AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ACC60948
                                                                                                                                                                                                                                                                                                                          Gavin
                                                                                                                                                      20-NOV-2002,
                                                                                                                                                                                                                                                                                                                          Bauer A, Ga
Marzioch M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a glucodextranase gene, the protein it encodes. The invention includes a method for the preparation of a polypeptide having glucodextranase activity in which a microbe transformed by a vector containing the gene is cultured and a polypeptide having glucodextranase activity is collected. The polypeptide can be used for the preparation of an isomalto-oligosaccharide. The present sequence represents the glucodextranase protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPQTSRVDGTIGQNGIQLDETAFPILLANQIGRTDAGFYRNELKPAAD-----YLVAAGP 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KNKFSGRYLVYGTFDYFLTAGAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTPQERW--EETGG--YSTSTLASQIAALAAADIAGKNGDAGSAAVYRA-----TADEW 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 FVLTLAIFGAASDN-----PIADRKCIVISDGDLVMHERKPGQEFPYYVYMIPKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 1047;
                        Glucodextranase gene and preparation of a polypeptide having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Indels
BRKPGQEFPYYVYMIPKG-TBYDDQRWILESVGGDHYKLKNKFSGRY
                                                                                                                                                                                                                                                                                                             Glucodextranase; isomalto-oligosaccharide; production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 QRSTEKWMFTINGPVGDGKYYLRISATGNPNDGATRDWG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 VREMDHFKFTAD --- GTGKYDISSKANGHPRSRG-KNWG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 79.5; I
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYDDQRWILESVGGDHYKL -------
                                                                                                                                                                                                                                                                      Glucodextranase amino acid sequence.
                                                                                                                                              AAB35740 standard; protein; 1047 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR52906 standard; protein; 1129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 8-11; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NISO ) NIPPON SHOKUHIN KAKO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-00056129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein sequence #SEQ ID 677.
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucodextranase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Conservative
                                                                                                                                                                                                                                                                                                                                                         Arthrobacter globiformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-615145/59.
N-PSDB; AAC66280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              JP2000245475-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-1999;
                                                                                                                                                                                                                              20-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2000.
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                                                                                                                                                                                         AAB35740;
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32; Gaps

56; Indels

DB 6; Length 1129;

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Kuester BD;

Kruse UD,

---PYYVYMIPK 56

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GKYIVEPLFDREALLTADLELAACDREKMTLDVTGHYSRPDLFHLEFRKQQ 309
                                                                                                                                                                                                                                                                                                                                                          fovel nitrilase polypeptide, useful for making (R) - or (S) -ethyl-4-cyano-
-hydroxybutyric acid or (R) - or (S)-mandelic acid or (S) - or (R)-phenyl
-actic acid derivative and for producing pharmaceutical composition, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to nitrilases and the nucleic acids that encode these enzymes thereof. Specifically, it refers to polypeptides that exhibit nitrilase activity, i.e. the ability to directly hydrolyse nitriles or cyanohydins into their corresponding carboxylic acids and ammonia. Nitrilases have commercial utility as biocatalysts for use in the synthesis of enantiomerically pure aromatic and aliphatic amino acids, as well as hydroxy acids, which are important for the development of chiral medicines. Furthermore, the present invention describes nitrilases, isolated from mesophilic microorganisms, that have improved activity and stability at inoreased ph and temperature. They are also inexpensive, efficient catalysts, have broad substrate specificity and are capable of chiral differentiation. This polypeptide is a protein sequence that exhibits nitrilase activity of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 ASDNPIADRKCIVISDGDLVMHBRKPGQBFPYYVYMIPKGTBYDDQRWILES----VGGD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                        ŭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Florida bitterbush, delta-6 fatty acid desaturase, tariric acid, transgenic plant, fatty acid, membrane-bound desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                        Chi
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                                                                                                                                                                                                                                                      Milan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Florida bitterbush delta-6 fatty acid desaturase.
                                                                                                                                                                                                                                                        Weiner DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 40; SEQ ID NO 244; 560pp; English
                                                                                                                                                                                                                                                        Chaplin JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY71551 standard; protein; 448 AA.
                                                                                                                                  21-JUN-2001; 2001US-0300189P.
30-JUL-2001; 2001US-0309006P.
22-JAN-2002; 2002US-0351336P.
                                                                                                   15-MAY-2002; 2002WO-US015983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                        Desantis G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 SGHIAGAG 317
                                                                                                                                                                                                      (DIVE-) DIVERSA CORP
                                                                                                                                                                                                                                                                                                        WPI; 2003-201417/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                         Burk M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 NGHPRSRG
                                                                                                                                                                                                                       (MADD/) MADDEN D.
                                                                                                                                                                                                                                                                                                                          N-PSDB; ADC23976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 332 AA;
                                WO2003000840-A2
                                                                                                                                                                                                                                                                                                                                                                                                             food additive.
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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                                                                   03-JAN-2003
                                                                                                                                                                                                                                                                        Short JM,
                                                                                                                                                                                                                                                        Madden M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY71551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
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ID AAY
XX AC AAY
XX DT 12-
XX XX Elc
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KW tre
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The present sequence is a delta-6 fatty acid desaturase protein sequence from clone pps.76001.63:ifs isolated from Florida bitterbush developing seed cDNA library, pps. The delta-6 desaturase enzyme catalyses the formation of tariric acid, a fatty acid that has a triple bond at the elta-6 carbon. The present sequence is useful for producing transgenic plants having altered levels of delta-6 desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polymucleotide is useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 ISDGDLVMHERKEPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKLKNKFSGRYLVYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISQADLAKH-KQPGD-----LWISIKGKVYDISKWTKEHPGGELPLL--SFAGGDVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                               Polymuclectide encoding delta-6 desaturase enzyme useful for produci
transgenic plants and for producing antibodies specific to which is
useful for screening cDNA expression libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 FDYFLT--AGAAVREMDHFKFTADGTGKYDISSKANGHPR--SRGKNWGVMK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - DARIAYHPGTAWQYLDRF-FTGYYVQDYSVSEMSKDYRLVSEFSKMGLFK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis; detection; pneumonia; otitis media; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.3%; Score 76.5; DB 3; Length 448; 28.6%; Pred. No. 8.9; tive 17; Mismatches 46; Indels 17
                                                                                                                                                                                                       Hitz WD, Kinney AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae SP0091 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "encoded by CTSC"
                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO 'E I.
                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 40-41; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW61216 standard; protein; 471 AA
                                                                                                            99WO-US028589
                                                                                                                                          98US-0110784P
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                                                                                                                                                                                                       Cahoon RE,
                                                                                                                                                                                                                                    WPI; 2000-412336/35.
                Picramnia pentandra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 32; Conserv
                                                                                                                                                                                                                                                     N-PSDB; AAD01349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 448 AA;
                                            WO200032790-A2.
                                                                                                                                          03-DEC-1998;
                                                                                                          02-DEC-1999;
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                                                                             08-JUN-2000
                                                                                                                                                                                                       Cahoon EB,
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Choi GH,
Rosen CA;
                                                                                                                                                           infection.
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Rosen CA;
 (DILL/)
(DOUG/)
(FANN/)
                                     ROSE/)
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                                                                                                                                                                                                     The present sequence represents a protein from Streptococcus pneumoniae. The uncleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against streptococcus pneumoniae, for inducing protective antibodies against streptococcus pneumonia, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the mucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunossays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 GAMMONEWLYDPAYSAYFYLKSDGT-YANQEW--QKVGGKWYYFKKWGYMARNEWQG--- 209
                                                                                                                               Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 GDLVMHERKPGQBFPYYVYMIPKGTEYDDQRWILESVGGDHYKLK-----NKFSGRYL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 VYGTFDYFLTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSRGKNWGVMKDGEKHYF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae; epitope; vaccine; antigenic protein; antibacterial; Streptococcal infection; detection.
                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 76; DB 2; Length 471;
; Pred. No. 11;
19; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. pneumoniae SP091 protein sequence SEQ ID NO:158
                                                                        Johnson LS, Hromockyj A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP54635 standard; protein; 471 AA
                                                                                                                                                                                 Claim 11; Page 81; 118pp; English
                        96US-0029960P
97WO-US019422
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                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae
                                                (HUMA-) HUMAN GENOME
                                                                        Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                              WPI; 1998-272224/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHOI/) CHOI G H.
(KUNS/) KUNSCH C A.
(BARA/) BARASH S C.
                                                                                                           N-PSDB; AAV27402
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 471 AA;
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30-OCT-1997;
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                        31-OCT-1996;
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                                                                        Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP54635;
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ABP54635
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vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polymuclectides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning of S. pneumoniae ORFS (open reading frames) which are used in an example
                                                                                                                                                                                                                                                                                                          New Streptococcus pneumoniae antigens, useful for detecting Streptococcus and for preventing or attenuating disease caused by Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 GAMMQNEWLYDPAYSAYFYLKSDGT-YANQEW--QKVGGKWYYFKKWGYMARNEWQG--- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 VYGTFDYFLTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSRGKNWGVMKDGEKHYF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 ----NYYLIGSGA---MATDEVIMDGTRYIFAASGELKEKKDINVGW-VHRDGKRYFF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The S.
                                                                                                                                             Fannon MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fannon MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 GDLVMHERKPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKLK------NKFSGRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ84792 to ABQ84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABP54557 to ABP54669. The pneumoniae antigens have antibacterial activity and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen; bacterial infection; vaccine; pneumonia; antibacterial.
                                                                                                                                                Dougherty B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dougherty B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.2%; Score 76; DB 5; Length 471;
25.2%; Pred. No. 11;
tive 19; Mismatches 48; Indels
                                                                                                                                           Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. pneumoniae antigenic protein SP091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC45239 standard; protein; 471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 42; 70pp; English.
                                                                                                                                             Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
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97US-00961083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2000; 2000US-00536784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.2*
....hes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae.
DILLON P J.
DOUGHERTY B.
FANNON M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunsch CA,
                                                                                                                                             Kunsch CA,
                                                                                                                                                                                                                         WPI; 2002-479261/51.
N-PSDB; ABQ84870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-764574/72
                                                                                    ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADC45238
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30-OCT-1997;
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                                                                                                    The invention relates to an isolated polynucleotide consisting of a Streptococcus pneumoniae nucleic acid (appearing as ADC45122 and encoding SP028) one of 113 disclosed nucleic acids encoding 113 S. pneumoniae antigens. Also included are making a recombinant vector by inserting the nucleic acid into a vector, an isolated polynucleotide consisting of at least 50 or 100 contiguous nucleotides of the SP028 nucleic acid, and a recombinant host cell comprising the SP028 polynucleotide. The nucleic acids are useful as DNA vaccine against Streptococcus pneumoniae infection (e.g. pneumonia). Nucleic acids derived from the S. pneumoniae antigen nucleic acids are useful as probes for use in diagnostic methods for detecting S. pneumoniae agene expression. The present sequence represents an S. pneumoniae antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 GAMMONEWLYDPAYSAYFYLKSDGT-YANOEW--OKVGGKWYYFKKWGYMARNEWGG--- 209
Novel polynucleotide encoding Streptococcus pneumoniae polypeptides useful for producing vaccines for prevention or attenuation of infection by Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 GDLVMHERKPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKLK-----NKFSGRYL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 VYGTFDYFLTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSRGKNWGVMKDGEKHYF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 ----NYYLTGSGA---MATDEVIMDGTRYIFAASGELKEKKDIANVGW-VHRDGKRYFF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS; bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism; kidney disease; diabetes; immunosuppressive disorder; otitis media; pneumococcal septicaemia; sinusitis; meningitis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                       22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a Streptococcus pneumoniae protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins and polynucleotides useful for diagnosis, prophylaxis of bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                             ; Score 76; DB 7; Length 471;
; Pred. No. 11;
19; Mismatches 48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae protein sequence ID51.
                                                                        Example 1; SEQ ID NO 158; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanniffy SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY81745 standard; protein; 490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 54; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                   9.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ91841
                                                                                                                                                                                                                                                                                                                                                 Sequence 471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200006738-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcal treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY81745;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
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fragments) are useful as immunogens or antigens. Immunogenic or antigenic compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or diagnostic assays. The sequences are useful for the detection or diagnostic of s. pneumoniae infection, by contacting a sample to be tested with them. Agents capable of antagonising, inhibiting or interfering with the function or expression of the protein or polypeptide are useful in medical compositions in the treatment or prophylaxis of S. pneumoniae infection. As the sequences can be used to treat S. pneumoniae infection, they can be used to treat bacterial pneumonia, which has high rates in young children, the elderly, and in patients with predisposing conditions such as asplenia, heart, lung and kidney disease, diabetes, alcoholism, or with immunosuppressive disorders, especially AIDS. They can also be used to treat pneumococcal septicaemia, otitis media, sinusitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMMONEWLYDPAYSAYFYLKSDGT-YANOEW--OKVGGKWYYFKKWGYMARNEWQG--- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GDLVMHERKPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKLK------NKFSGRYL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 VYGTFDYFLTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSRGKNWGVMKDGEKHYF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----NYYLTGSGA---MATDEVIMDGTRYIFAASGELKEKKDLMVGW-VHRDGKRYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a protein comprising or having at least 50° identity to any of the 2469 amino acid sequences, identified in the
derivatives and/or

    gneumoniae type 4 strain protein from coding region #1611.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           % Match 9.2%; Score 76; DB 3; Length 490; Local Similarity 25.2%; Pred. No. 12; les 30; Conservative 19; Mismatches 48; Indels
nvention. The proteins (or their homologues,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; type 4 strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3222; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU02034 standard; protein; 506 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 490 AA;
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11-FEB-2003
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specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the mucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target composition, a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence and where the parts of the primers having substantial complementary to complement of the complement of the target sequence to be amplified, assay comprising contacting a test compound with the beam of actorian and determining whether the test compound binds to the protein protein, and determining whether the test compound binds to the protein card molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus conding the proteins and antibiotics. The methods are useful for identifying watchers, but was obtained sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat figured on 23-0CT-2003 to
               $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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# Sequence 506 AA;

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34 GDLVMHERKPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKLK-----NKFSGRYL 86
                                                                                                                                                                                            87 VYGTFDYFLTAGAAVREMDHFKFTADGTGKYDISSKANGHPRSRGKNWGVMKDGEKHYF 145
                                             22; Gaps
Query Match 9.2%; Score 76; DB 6; Length 506; Best Local Similarity 25.2%; Pred. No. 12; Matches 30; Conservative 19; Mismatches 48; Indels
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#### AAG38201 standard; protein; 179 AA. AAG38201; RESULT 15 AAG38201

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 47094.

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thaliana.

25-FEB-2000; 2000EP-00301439 EP1033405-A2, 06-SEP-2000.

25-FEB-1999; 05-MAR-1999 23-MAR-1999

99US-0121825P. 99US-0123180P. 99US-0125548P. 99US-0125788P. 99US-0126785P. 99US-0126785P. 25-MAR-1999; 29-MAR-1999; 01-APR-1999;

99US-0139459P. 99US-0139460P. 99US-0139461P. 99US-0139462P. 99US-0130449P 99US-0132407P 99US-0132484P 99US-0132486P 99US-0132487P 99US-0134941P 99US-0135124P 99US-0136782P 99US-0137502P 99US-0138847P 99US-0139452P 99US-0139453P. 99US-0139454P 99US-0139455P. 99US-0139457P. 99US-0139458P 99US-0139750P. 99US-0139763P. 99US-0139899P. 99US-0140353P. 99US-0140354P. 99US-0140823P. 99US-0136392P 99US-0140991P. 99US-0141287P 99US-0142154P 99US-0142055P 99US-0141842P 99US-0142390P 99US-0142803P 99US-0142920P 9US-0143624P 9US-0144005P 99US-0144086P 99US-0144331P 99US-01 21-APR-1999 23-APR-1999 19-JUL-1999; 04-JUN-1999 6-JUN-1999

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9905-0144332P-9905-0144333P-9905-0144333P-9905-0144333P-9905-0144332P-9905-0144632P-9905-0144632P-9905-0144632P-9905-014508P-9905-014508P-9905-014508P-9905-014508P-9905-014503P-9905-014503P-9905-014503P-9905-014503P-9905-014503P-9905-014503P-9905-014503P-9905-014503P-9905-014933P-9905-014933P-9905-014933P-9905-014933P-9905-014933P-9905-014933P-9905-014933P-9905-014933P-9905-014933P-9905-014933P-9905-014933P-9905-015089P-9905-015089P-9905-015089P-9905-015089P-9905-015089P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-015373P-9905-01537
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28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
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05-AUG-1999;
05-AUG-1999;
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26-AUG-1999;
27-AUG-1999;
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07-SEP-1999;
10-SEP-1999;
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15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
23-SEP-1999;
24-SEP-1999;
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12-OCT-1999;
13-OCT-1999;
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16-AUG-1999
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------GDHYKLKNKFSGRYLVYGTFDYFLTA--GAAVREMDHFKFTADG 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | : | | | | :: | IVISNRDLFWAPITVGD------VVPDGTISFFDENDQLQTVSVHSIAAGKKVILFGVP
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                 990S-01592959-
990S-0159331P-
990S-0159331P-
990S-0159331P-
990S-0159638P-
990S-016741P-
990S-0160741P-
990S-0160741P-
990S-0160741P-
990S-0160981P-
990S-0160981P-
990S-0160981P-
990S-0161981P-
990S-0161931P-
990S-0161359P-
990S-0161359P-
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Search completed: September 9, 2004, 15:28:08 Job time : 126 secs

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(without alignments)
380.819 Million cell updates/sec
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1 MSITQSFFVLTLAIFGAASD......NWGVMKDGEKHYFTVENCQE 152
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2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/RCT_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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3: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

			Appli	Appli	Appli	App11	Appli	App1	Appli	App1	Appli	App1	Appli	Appli	7. Appl	Appli	193032,
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o\f	Query	Match	100.0	100.0	100.0	73.9	73.9	73.9	15.8	15.8	15.8	10.5	10.5	10.5	9.6	9.8	9.5
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	Sequence 244, App Sequence 244, App	Sequence 244, App	Sequence 244, App	Sequence 158, App	Sequence 98, Appl	Sequence 13, Appl	Sequence 3, Appli	Sequence 6, Appli	Sequence 74789, A	Sequence 2112, Ap	Sequence 15, Appl	Sequence 379, App	Sequence 2113, Ap	Sequence 206, App			Sequence 190303,		Sequence 175079,	Sequence 175053,			107,	Sequence 1849, Ap	Sequence 1849, Ap	Sequence 5, Appli	Sequence 71100, A
US-10-369-493-1 US-10-440-503-2	.Z US-10-461-925-244 .4 US-10-146-772-244	.5 US-10-241-742-244	.5 US-10-440-523-244	US-09-765-272-158	.0 US-09-769-744A-98	.6 US-10-229-148B-13	US-09-870-472-3	US-09-870-472-6	.2 US-10-282-122A-74789	.6 US-10-408-765A-2112	.4 US-10-205-194-15	.6 US-10-408-765A-379	.6 US-10-408-765A-2113	.6 US-10-408-765A-206	.6 US-10-408-765A-207	.2 US-10-282-122A-65010	.6 US-10-437-963-190303	.4 US-10-156-761-10627	16 US-10-437-963-175079		12 US-10-282-122A-51283	.2 US-10-282-122A-46513	14 US-10-043-344-107	.0 US-09-880-748-1849	12 US-10-293-418-1849	US-09-969-362-5	12 US-10-282-122A-71100
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17	19	20	21	22	23	24	22	26	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45
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# ALIGNMENTS

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61 DDQRWILESVGGDHYKLKNKFSGRYLVYGTFDYFLTAGAAVREMDHFKFTADGTGKYDIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DDQRWILESVGGDHYKLKUKFKSGRYLVYGTFDYFLTAGAAVREMDHFKFTADGTGKYDIS 120
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Sequence 2, Application US/10218699
| Publication No. US20030012795A1
| GENERAL INFORMATION:
| APPLICANT: Cupp, Mary S. |
| APPLICANT: Cupp, Mary S. |
| APPLICANT: Cupp, Eddie W. |
| APPLICANT: Swaim, Steven F. |
| TITLE OF INVENTION: Recombinant Vasoactive Protein from |
| TITLE OF INVENTION: Salivary Gland of the Black Fly |
| CURRENT APPLICATION NUMBER: US/10/218,699 |
| CURRENT APPLICATION NUMBER: US/10/218,699 |
| CURRENT FILING DATE: 2002-08-14 |
| PRIOR FILING DATE: 2000-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SKANGHPRSRGKNWGVMKDGEKHYFTVENCQE 152
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 5
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Simulium vittatum
US-10-218-699-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 152; Conservative
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SEQ ID NO 2
LENGTH: 152
TYPE: PRT
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LENGTH: 109
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                                                                                                                         ublication No. CELLON:
GENERAL INFORMATION:
Ribeiro, Jose M.C.
Cupp, Acidie W.
Swaim, Steven F.
Swaim, Steven F.
SYAIM, Steven F.
SAILVARY GLAND OF THE BLACK FLY
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIR:
APPLICATION INVIER: US/10/288,740
FILING DAIE: 06-No. US20030109447A1-2002
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/036,355A
FILING DATE: 06-WARCH-1998
ATTORNSY AGENT INFORMATION:
NAME: SPILIN W. MURIEN: 32,943
REGISTRATION UNDERR: 32,943
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 919 831 3175
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
121 SKANGHPRSRGKNWGVMKDGEKHYFTVENCOE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKANGHPRSRGKNWGVMKDGEKHYFTVENCOE 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 152 amino acids TYPE: amino acid
                                                                                                     Sequence 2, Application US/10288740 Publication No. US20030109447A1
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Matches 152; Conservative
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                                                             RESULT 2
US-10-288-740-2
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DDQRWILESVGGDHYKLKNKFSGRYLVYGTFDYFLTAGAAVREMDHFKFTADGTGKYDIŞ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Cupp, Mary S.
APPLICANT: Cupp, Mary S.
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Gwaim, Steven F.
TITLB OF INVENTION: Recombinant Vascactive Protein from
TITLE OF INVENTION: Salivary Gland of the Black Fly
FILE REFERENCE: 35721/205407
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: US/09/702,647
PRIOR PLING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Cupp, Eddie W.
APPLICANT: Cupp, Eddie W.
TITLE OF INVENTION: Recombinant Vasoactive Protein from
TITLE OF INVENTION: Recombinant Vasoactive Protein from
TITLE OF INVENTION: Ralivary Gland of the Black Fly
FILE REFERENCE: 35721/205407
CURRENT APPLICATION NUMBER: US/10/768,874
CURRENT PLILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: US/10/218,699
PRIOR PILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 152; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKANGHPRSRGKNWGVMKDGEKHYFTVENCQE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SKANGHPRSRGKNWGVMKDGEKHYFTVENCQE 152
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Publication No. US20030012795A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Simulium vittatum
US-10-218-699-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Simulium vittatum
US-10-768-874-2
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Sequence 2, Application US/10768874 Publication No. US20040142869A1 GENERAL INFORMATION: APPLICANT: Cupp, Mary S.

US-10-768-874-2

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42 KPGQEFPYYVYMIPKGTEYDDQRWILESVGGDHYKLKNKFSGRYLVYGTFDYFLTAGAAV 101
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                                                                                                                                                                                                      Swalm, Steven F.
TITLE OF INVENTION: RECOMBINANT VASOACTIVE PROTEIN FROM
SALIVARY GLAND OF THE BLACK FLY
                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSER: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 27622

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/288,740
FILING DATE: 06-No. US20030109447A1-2002
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/10768874
Publication No. US20040142869A1
GENERAL INFORMATION:
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Cupp, Mary S.
APPLICANT: Cupp, Bddie W.
APPLICANT: Supp, Steven F.
APPLICANT: Sawim, Steven F.
TITLE OF INVENTION: Recombinant Vascactive Protein from TITLE OF INVENTION: Salivary Gland of the Black Fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/036,355A
FILING DATE: 06-MARCH-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5721-4
TELECOMMUNICATION INPORMATION:
TELEFRAME: 919 420 2202
TELEFRAME: 919 841 3175
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-288-740-5
                                                                                                                        APPLICANT: Cupp, Mary S.
Ribeiro, Jose M.C.
Cupp, Eddie W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                ; Sequence 5, Application US/10288740 ; Publication No. US20030109447A1
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                             GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                     US-10-288-740-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-10-768-874-5
RESULT 5
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1 KPGQEFPYYVYMIPKGTBYDDQRWILESVGGDHYKLKNKFSGRYLVYGTFDYFLITAGAAV 60
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                                                                                                                                                                                                                                                                                                                                                             Length 109;
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Cupp, Eddie W.
Swaim, Steven F.
TITLE OF INVENTION: RECOMBINANT VASOACTIVE PROTEIN FROM
SALIVARY GLAND OF THE BLACK FLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.8%; Score 130; DB 14; Length 22; 100.0%; Pred. No. 9.9e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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; Publication No. US20030012795A1
; GENERAL INFORMATION;
; APPLICANT: CUPP, Mary S.
; APPLICANT: CUPP, Mary S.
; APPLICANT: CUPP, Eddie W.
; TITLE OF INVENTION: Recombinant Vascactive Protein from TITLE OF INVENTION: Salivary Gland of the Black Fly FILE REFERENCE: 35721/205407
; FILE REFERENCE: 35721/205407
; CURRENT APPLICATION NUMBER: US/10/218,699
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US/09/702,647
; PRIOR PILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
: LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                        Query Match 73.9%; Score 610; DB 16; Best Local Similarity 100.0%; Pred. No. 5.8e-62; Matches 109; Conservative 0; Mismatches 0;
              CURRENT APPLICATION NUMBER: US/10/768,874
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: US/10/218,699
PRIOR FILING DATE: 2002-08-14
PRIOR PLING DATE: 2000-10-31
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PastSEQ for Windows Version 4.0
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FILE REFERENCE: 35721/205407
                                                                                                                                                                                                                                                                                ) ORGANISM: Simulium vittatum
US-10-768-874-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Simulium vittatum US-10-218-699-3
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Best Local Similarity 100.0
Matches 22; Conservative
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LENGTH: 109
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S-10-288740,
S-20-288740,
Sublication US/10288740
Sublication No. US20030109447A1
GENERAL INPORMATION:
GENERAL INPORMATION:
Cupp, Mary S.
Cupp, Bddie W.
Cupp, Bddie W.
TITLE OF INVENTION: RECOMBINANT VASOACTIVE PROTEIN FROM
SALIVARY GLAND OF THE BLACK FLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OB 14; here,
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CORRESPONDENCE ADDRESS:
ADDRESSES W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
                                                                                                                                                                                                    Sequence 4, Application US/10218699;
Publication No. US20030012795A1
GENERAL INFORMATION:
APPLICANT: Cupp, March N.C.
APPLICANT: Cupp, Eddie W.C.
APPLICANT: Cupp, Eddie W.C.
TITLE OF INVENTION: Recombinant Vascactive Protein from TITLE OF INVENTION: Recombinant Vascactive Protein from TITLE OF INVENTION: Recombinant Vascactive Protein from TITLE OF INVENTION: Salivary Gland of the Black Fly CURRENT FILING DATE: 108/10/218,699
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-10-31
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/288,740
FILING DATE: 06-No. US20030109447A1-2002
CLASSIFICATION: 514
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ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 15; Conservative 0; Mismatches
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 15
                                             131 GKNWGVMKDGEKHYFTVENCQE 152
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                               1 GKNWGVMKDGEKHYFTVENCOE
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22; Conservative
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                                                                                                                                                                                             US-10-218-699-4
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Matches
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                                                                                                                                       ZIP: 27622
COMPUTER READBELE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
    APPLICATION DATE: US/10/288,740
FILING DATE: 06-No. US20030109447A1-2002
CLASSIFICATION: 514
                    ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cupp, Mary S.
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Cupp, Eddie W.
APPLICANT: Swaim, Steven F.
TITLE OF INVENTION: Recombinant Vasoactive Protein from TITLE OF INVENTION: Salivary Gland of the Black Fly FILE REFERENCE: 3571/205407
CURRENT APPLICATION NUMBER: US/10/768,874
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: US/0/218,699
PRIOR APPLICATION NUMBER: US/09/702,647
PRIOR APPLICATION NUMBER: US/09/702,647
PRIOR SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 22
THENTH: 22
THENTH: DATE: 200-10-31
THENTH: 22
THENTH: 22
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/036,355A

PILING DATE: OG-MARCH-1998

ATTORNEY/AGENT INFORMATION:

NAME: SPINILL, W. MURTAY

REGISTRATION UNDERS: 32,943

REFERENCE/DOCKET NUMBER: 5721-4

TELECOMMUNICATION INFORMATION:

TELEPAX: 919 881 3175

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 GKNWGVMKDGEKHYFTVENCOE 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT; ORGANISM: Simulium vittatum
US-10-768-874-3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYPE: amino acid
                                                                  CITY: Raleigh
                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 22; Conserva
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Best Local Similarity
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us-10-768-874-2.rapb

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US-10-790-396-7
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                                                                                                                                                          SEQ ID NO 17
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Best Local 8
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APPLICANT: Ribeiro, Jose M.C.
APPLICANT: Cupp, Mary S.

APPLICANT: Cupp, Mary S.

APPLICANT: Cupp, Mary S.

TITLE OF INVENTION: Recombinant Vasoactive Protein from TITLE OF INVENTION: Ralivary Gland of the Black Fly CURRENT APPLICATION NUMBER: US/10/18,699

PRIOR APPLICATION NUMBER: US/10/18,699

PRIOR FILING DATE: 2002-08-14

PRIOR FILING DATE: 2000-10-31

PRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yang, Shumin
APPLICANT: Yang, Shumin
APPLICANT: Sellins, Karen S.
ITILE OF INVENTION: NOVEL PORMS OF T CELL COSTIMULATORY
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-1-C1-PCT
CURRENT PELLORION NUMBER: US/10/790,396
CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/09/646,561
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5721-4
TELECOMMATCATION INFORMATION:
TELEPHONE: 919 420 2202
TELEPHONE: 919 420 2202
TELEPHONE: 919 881 3175
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 17, Application US/10790396; Publication No. US20040157296A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/10768874; Publication No. US20040142869A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  42 KPGQEFPYYVYMIPK 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Simulium vittatum
US-10-768-874-4
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
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US-10-790-396-17
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PROTEINS, NUCLEIC
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7 MBLNNILFVWTLLLYGAASWKSQAYFNKTGELPCHFTNSQNISLDELVVFWQDQDKLVLY 66
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7 MELNNILFVWTLLLYGAASWKSQAYFNKTGELPCHFTNSQNISLDELVVFWQDQDKLVLY 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 ELYRGKENPQNVHRKYKGRTSFDKDNWTLRL----HNIQIKDKGLY 108
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APPLICANT: Yang, Shaunan
APPLICANT: Yang, Shaunan
APPLICANT: Sellins, Karen S.
TITLE OF INVENTION: NOVEL PORNS OF CELL COSTIMULATORY PR
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REPERENCE: IM-1-C1-PCT
CURRENT PEPLICATION NUMBER: US/09/646,561
PRIOR APPLICATION NUMBER: US/09/646,561
PRIOR APPLICATION NUMBER: 09/09/19
PRIOR APPLICATION NUMBER: 09/079,765
PRIOR APPLICATION NUMBER: 09/079,765
PRIOR APPLICATION NUMBER: 09/062,597
PRIOR PLICATION NUMBER: 09/062,597
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9.8%; Score 80.5; DB 16;
Best Local Similarity 27.1%; Pred. No. 1.3;
Matches 29; Conservative 13; Mismatches 38;
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/078,765
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 09/062,597
PRIOR APPLING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 7, Application US/10790396
; Publication No. US20040157296A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
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ORGANISM: Canis familiaris
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 193032
LENGTH: 721
TYPE: PRT
CURRENT PRESENCE: ACID MOS: 204966
SEQ ID NO 193032
CURRENT SEQ ID NOS: 204966
SEQ ID NO 193032
CURRENT SECTION OF ACID MOS: 204966
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9.5%; Score 78.5; DB 16; Length 721;
Best Local Similarity 25.6%; Pred. No. 7.8;
Matches 30; Conservative 21; Mismatches 53; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
| NAME/KRY: unsure
| LOCATION: (1). (721)
| OTHER INFORMATION: unsure at all Xaa locations
| PEATURE:
| OTHER INFORMATION: Clone ID: PAT_MRT4530_89208C.1.pep
US-10-437-963-193032
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Search completed: September 9, 2004, 15:42:38 Job time : 129 secs